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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:24:27 ; Search time 12.1667 Seconds
(without alignments)
631.182 Million cell updates/sec

Title: US-09-931-186-20

Sequence: 1 NMAACRSVAGLVAVITGAS.....ENPFLNGEIVRLDAIRMQP 261

Scoring table: BLOSUM62
Gapco 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: Issued Patents AA: *
2: /cgn2_6/prodata/1/aa/5A.COMB.pep: *
3: /cgn2_6/prodata/1/aa/5B.COMB.pep: *
4: /cgn2_6/prodata/1/aa/5A.COMB.pep: *
5: /cgn2_6/prodata/1/aa/5B.COMB.pep: *
6: /cgn2_6/prodata/1/aa/PCITUS.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1300	99.7	261	4	US-08-815-225-2
2	1300	99.7	261	4	US-08-815-225-3
3	1300	99.7	261	4	US-09-347-878-50
4	666.5	51.1	388	4	US-08-980-832-41
5	328.5	25.2	243	4	US-09-239-052-2
6	302	23.2	255	4	US-08-815-225-4
7	300.5	23.0	333	1	US-08-815-225-4
8	298	22.9	263	4	US-09-134-001C-4512
9	296.5	22.7	262	4	US-09-563-189B-6
10	294	22.5	315	3	US-08-793-035-9
11	294	22.5	315	3	US-08-793-035-10
12	287.5	22.0	244	1	US-08-375-962B-13
13	287.5	22.0	244	2	US-08-562-114B-13
14	287.5	22.0	244	4	US-08-729-594A-13
15	287.5	22.0	244	4	US-08-937-993-13
16	287.5	22.0	246	6	5512669-4
17	282.5	21.7	273	6	529279-7
18	280.5	21.5	274	4	US-09-134-001C-4431
19	275.5	21.1	249	4	US-09-134-001C-4825
20	271.5	20.8	246	3	US-09-238-481-2
21	271.5	20.8	246	4	US-09-572-810A-2
22	269	20.6	231	4	US-09-134-001C-4597
23	268.5	20.6	337	1	US-08-440-856A-3
24	267	20.5	186	4	US-08-858-207A-270
25	267	20.5	256	4	US-09-504-358-14
26	267	20.5	256	4	US-09-954-314-14
27	266	20.4	247	1	US-08-241-766-13

28	258	19.8	261	4	US-09-468-738A-29	Sequence 29, Appl
29	258	19.8	261	4	US-09-940-019-29	Sequence 29, Appl
30	255.5	19.6	263	6	5229279-4	Patent No. 5229279
31	253.5	19.4	263	4	US-09-134-001C-3505	Sequence 3505, Ap
32	252.5	19.4	257	4	US-09-134-001C-3562	Sequence 3562, Ap
33	251.5	19.3	252	3	US-08-822-332-8	Sequence 8, Appl
34	251.5	19.3	252	4	US-09-466-109-8	Sequence 8, Appl
35	246	18.9	256	1	US-08-559-808B-7	Sequence 8, Appl
36	243	18.6	271	2	US-07-637-885-2	Sequence 8, Appl
37	243	18.6	359	1	US-08-440-856A-8	Sequence 8, Appl
38	240	18.4	258	4	US-09-504-358-12	Sequence 12, Appl
39	240	18.4	292	4	US-09-954-314-12	Sequence 12, Appl
40	240	18.4	292	3	US-09-109-205-2	Sequence 2, Appl
41	240	18.4	292	4	US-09-443-184-8	Sequence 58, Appl
42	231.5	17.8	251	3	US-08-822-332-9	Sequence 9, Appl
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44	225	17.3	283	4	US-09-367-012-1	Sequence 1, Appl
45	225	17.3	283	4	US-09-777-157A-1	Sequence 5042, Ap
46	216	16.6	267	4	US-09-134-001C-5042	Sequence 5346, Ap
47	211	16.2	283	4	US-09-134-001C-5346	Sequence 9, Appl
48	208	16.0	313	4	US-09-413-814-8	Sequence 4339, Ap
49	207	15.9	290	4	US-09-134-001C-4339	Sequence 2, Appl
50	204	15.6	248	2	US-09-099-367-2	Sequence 11, Appl
51	189	14.5	248	4	US-09-385-068-11	Sequence 2, Appl
52	186.5	14.3	292	4	US-09-468-738A-2	Sequence 2, Appl
53	186.5	14.3	292	4	US-09-940-019-2	Sequence 5, Appl
54	186.5	14.3	295	3	US-09-002-298-5	Sequence 23, Appl
55	186.5	14.3	296	4	US-09-468-738A-23	Sequence 39, Appl
56	186.5	14.3	296	4	US-09-940-019-23	Sequence 39, Appl
57	186.5	14.3	318	4	US-08-729-554A-39	Sequence 39, Appl
58	186.5	14.3	318	4	US-08-937-993-39	Sequence 39, Appl
59	185	14.2	244	1	US-08-762-129-4	Sequence 2864, Ap
60	182.5	14.0	272	4	US-09-134-001C-2864	Sequence 4059, Ap
61	182.5	14.0	295	4	US-09-134-001C-4059	Sequence 3, Appl
62	182	14.0	244	1	US-08-762-129-3	Sequence 2, Appl
63	182	14.0	257	4	US-09-287-097-2	Sequence 2, Appl
64	182	14.0	295	4	US-09-026-482B-2	Sequence 15, Appl
65	181.5	13.9	318	2	US-08-562-114B-15	Sequence 15, Appl
66	181.5	13.9	318	3	US-09-109-205-17	Sequence 15, Appl
67	181.5	13.9	318	4	US-08-729-554A-15	Sequence 1, Appl
68	181.5	13.9	318	4	US-09-880-427-1	Sequence 1, Appl
69	181.5	13.9	318	4	US-09-306-538B-1	Sequence 1, Appl
70	181.5	13.9	318	4	US-08-937-993-15	Sequence 15, Appl
71	180.5	13.8	318	4	US-08-375-962B-14	Sequence 14, Appl
72	180.5	13.8	318	4	US-08-940-424-3	Sequence 3, Appl
73	175.5	13.5	244	1	US-08-762-129-1	Sequence 38, Appl
74	174	13.3	318	4	US-08-729-554A-38	Sequence 38, Appl
75	174	13.3	301	4	US-09-937-993-38	Sequence 98, Appl
76	173	13.3	301	4	US-09-288-143-98	Sequence 37, Appl
77	172	13.2	303	3	US-09-002-288-1	Sequence 37, Appl
78	166.5	12.8	317	4	US-08-729-554A-37	Sequence 37, Appl
79	166.5	12.8	317	4	US-08-937-993-37	Sequence 21, Appl
80	162	12.4	255	4	US-09-036-967A-21	Sequence 21, Appl
81	162	12.4	255	4	US-09-370-700-21	Sequence 1, Appl
82	161.5	12.4	319	2	US-08-977-847-1	Sequence 1, Appl
83	161.5	12.4	319	2	US-09-195-021-1	Sequence 18, Appl
84	160.5	12.3	317	3	US-09-109-205-18	Sequence 5, Appl
85	160.5	12.3	317	4	US-08-940-424-5	Sequence 2, Appl
86	160.5	12.3	360	4	US-09-740-028A-2	Sequence 7, Appl
87	159.5	12.2	274	4	US-09-740-028A-4	Sequence 36, Appl
88	159.5	12.2	335	3	US-09-002-298-7	Sequence 36, Appl
89	158.5	12.0	316	4	US-08-729-554A-36	Sequence 6, Appl
90	156.5	12.0	316	4	US-08-937-993-36	Sequence 19, Appl
91	156.5	12.0	335	3	US-09-109-205-19	Sequence 3, Appl
92	156.5	11.8	335	3	US-08-977-847-3	Sequence 3, Appl
93	152.5	11.7	317	2	US-09-195-021-3	Sequence 4, Appl
94	152.5	11.7	317	2	US-08-940-424-4	Sequence 339, App
95	152.5	11.7	318	4	US-09-605-785-339	Sequence 339, App
96	152	11.7	318	4	US-09-439-313-339	Sequence 339, App
97	152	11.7	318	4	US-09-352-616A-339	Sequence 12, Appl
98	152	11.7	318	4	US-08-375-962B-12	
99	152	11.7	318	4		
100	151	11.6	327	1		

ALIGNMENTS

RESULT 1
US-08-815-225-2; Sequence 2, Application US/08815225
; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-815-225-2

Query Match 99.7%; Score 1300; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.7e-136;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MAACRSVKGVAIVTTGGASGLGATAEKLVGASAVLDDLPNSGGGAQAKKIGNCVF 60
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QY 61 APADVTSEKDVOTALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDV 120
    |||||||
DB 61 APADVTSEKDVOTALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDV 120
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DB 181 PIARDLAPIGIRVMTIAPGLFGLTSLPEKVANFLASQVFPFRLGDPAEYAHVQAI 240
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QY 241 IENPFLNGEVIRLDGAIRMOP 261
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DB 241 IENPFLNGEVIRLDGAIRMOP 261
    |||||||
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RESULT 2

US-08-815-225-3

; Sequence 3, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-815-225-3

Query Match 99.7%; Score 1300; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.7e-136;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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    |||||||
DB 61 APADVTSEKDVOTALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDV 120
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QY 121 NLMGTFNVRILVAEGKQNEPDGQGRGVITNTASVAAPFEGVGOAAVSASKGGIVGNTL 180
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DB 121 NLMGTFNVRILVAEGKQNEPDGQGRGVITNTASVAAPFEGVGOAAVSASKGGIVGNTL 180
    |||||||
QY 181 PIARDLAPIGIRVMTIAPGLFGLTSLPEKVANFLASQVFPFRLGDPAEYAHVQAI 240
    |||||||
DB 181 PIARDLAPIGIRVMTIAPGLFGLTSLPEKVANFLASQVFPFRLGDPAEYAHVQAI 240
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QY 241 IENPFLNGEVIRLDGAIRMOP 261
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DB 241 IENPFLNGEVIRLDGAIRMOP 261
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RESULT 3

US-09-347-878-50

; Sequence 50, Application US/09347878C

; Patent No. 6376210

; GENERAL INFORMATION:

; APPLICANT: Yuan, Chong

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
;; FILE REFERENCE: 25885-1651
;; CURRENT APPLICATION NUMBER: US/09/347,878C
;; CURRENT FILING DATE: 1999-07-06
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 50
;; LENGTH: 261
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-347-878-50

Query Match 99.7%; Score 1300; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.7e-136;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 MAAACRSVKGLVAVITGGASGLIATAERLVGGASAVLLDLPNSGGEAOKKGNVCYF 60
Db 1 MAAACRSVKGLVAVITGGASGLIATAERLVGGASAVLLDLPNSGGEAOKKGNVCYF 60
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61 APADVTSEKDVOTATLAKGKFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDV 120
Db 61 APADVTSEKDVOTATLAKGKFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDV 120
QY 121 NLGTFENVIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTL 180
121 NLGTFENVIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTL 180
Db 121 NLGTFENVIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTL 180
QY 181 PIADLAPIGIRVWTIAPGLFGLPLTSLPEKYNFLASQVPPSRIGDAEVAHLVQAI 240
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Db 181 PIADLAPIGIRVWTIAPGLFGLPLTSLPEKYNFLASQVPPSRIGDAEVAHLVQAI 240
QY 241 IENFNGEYIRLDGAIRMP 261
241 IENFNGEYIRLDGAIRMP 261
Db 241 IENFNGEYIRLDGAIRMP 261

RESULT 4

US-08-980-832-41
; Sequence 41, Application US/08980832B
; Patent No. 6291204
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tsygankov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/08/980,832B
; CURRENT FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 41
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Flavobacterium sp. R1534
US-08-980-832-41

Query Match 51.1%; Score 666.5; DB 4; Length 388;
Best Local Similarity 55.5%; Pred. No. 1.7e-65;

Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

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8 VKGLVAVITGGASGLIATAERLVGGASAVLLDLPNSGGEAOKKGNVCYFAPADVT 67
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143 IEGRVFVVTGAASGLGASASARMLAOGGAKVYIADL-----AEPKDAPEGAVHAACDVT 196
QY 68 EKDVOTATLAKGKFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDVNLGTFNV 127
68 EKDVOTATLAKGKFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDVNLGTFNV 127
Db 197 ATAQOTATLAKGKFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDVNLGTFNV 254
197 ATAQOTATLAKGKFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDVNLGTFNV 254
QY 128 VIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTLPIARDLA 187
128 VIRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTLPIARDLA 187
Db 255 MARLAARMAARNEVVR-GERGVAVNTASIAAODQIQCAVAYASKSGVAGNTLPMARDLA 313
255 MARLAARMAARNEVVR-GERGVAVNTASIAAODQIQCAVAYASKSGVAGNTLPMARDLA 313
QY 188 PIGIRVWTIAPGLFGLPLTSLPEKYNFLASQVPPSRIGDAEVAHLVQAIENFNLN 247
188 PIGIRVWTIAPGLFGLPLTSLPEKYNFLASQVPPSRIGDAEVAHLVQAIENFNLN 247

Db 314 RHGIRVWTIAPGLFGLPLTSLPEKYNFLASQVPPSRIGDAEVAHLVQAIENFNLN 373
314 RHGIRVWTIAPGLFGLPLTSLPEKYNFLASQVPPSRIGDAEVAHLVQAIENFNLN 373
QY 248 GEVIRLDGALRMAP 387
248 GEVIRLDGALRMAP 387
Db 374 GEVIRLDGALRMAP 387

RESULT 5

US-09-239-052-2
; Sequence 2, Application US/09239052
; Patent No. 6346395

GENERAL INFORMATION:

APPLICANT: Holmes, David J.
APPLICANT: Zhong, Yiyi
APPLICANT: Debouck, Christine
APPLICANT: Jaworski, Deborah D.
APPLICANT: Wang, Min
APPLICANT: Warren, Richard L.
APPLICANT: Kosmetka, Anna L.
APPLICANT: McDevitt, Damien
APPLICANT: Ingram, Karen A.
APPLICANT: Chalker, Allison F.
APPLICANT: So, Chi Young
APPLICANT: Wallis, Nicola G.
APPLICANT: Pearson, Stewart C.
TITLE OF INVENTION: FAbG
FILE REFERENCE: GM10191
CURRENT APPLICATION NUMBER: US/09/239,052
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 25.2%; Score 328.5; DB 4; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.5e-28;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

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15 ITGGASGLIATAERLVGGASAVLLDLPNSGGE-----AOKKGNVCYFAPADVTSE 68
Db 10 ITGSSSGIGLAIHFAAGANIVL---NSGAISEELAEFSYGRVPIGSDVDF 65
10 ITGSSSGIGLAIHFAAGANIVL---NSGAISEELAEFSYGRVPIGSDVDF 65
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69 KIVOTATLAKGKFGVAVVAVNCAGIAVASKTYNKKQOTHTLEDFQVLDVNLGTFNV 128
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66 ADARKMIDQAIHLESDVYLVNNAI--TQDTLMK-----TEADFEKLVKNLGAIRNM 119
QY 129 IRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTLPIARDLA 188
129 IRLVAGEMQNEPDGQGRGVIIINTASVAAREGQVQAAYSASKGIYGMTLPIARDLA 188
Db 120 TOSVL-----KPMKARCGATINNSVVGMLGNIGNQANYASKGLIGFTSVAREVAS 173
120 TOSVL-----KPMKARCGATINNSVVGMLGNIGNQANYASKGLIGFTSVAREVAS 173
QY 189 IGIRVWTIAPGLFGLPLTSLPEKYNFLASQVPPSRIGDAEVAHLVQAIENFNLN 248
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Db 174 RNIRVAVIAPGMIESMRAILSDKIKETIAQIPM-KERGAQVYADLVFLAGQDYILNG 232
174 RNIRVAVIAPGMIESMRAILSDKIKETIAQIPM-KERGAQVYADLVFLAGQDYILNG 232
QY 249 EVIRLDGALRMAP 259
249 EVIRLDGALRMAP 259
Db 233 OVIALDGLISM 243

RESULT 6

US-08-815-225-4
; Sequence 4, Application US/08815225
; Patent No. 6268479

GENERAL INFORMATION:

APPLICANT: Stern, David M.
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
NEURODEGENERATIVE CONDITIONS

Thu Jun 26 06:55:04 2003

us-09-931-186-20.ra1

Page 4

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NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55209
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-815-225-4

Query Match      23.2% Score 302; DB 4; Length 255;
Best Local Similarity 33.6% Pred. No. 2.3e-25;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;

QY 8 VGLVAVITGASGGLTAERLVGOGASAVLLDLPNSGGEQAOKKLGNNCFAPADVT 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 LSKRTVITGARGGLAEARQAVAGARVVLADVLDEGATFARLGPARYOHLDTVI 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 EKDVQALALAKGKEQDVAVANCAGIYASKTYNLKKGQHTLEDFQVLDVNLMTFN 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 EEWQWYVAVAREFESVDGLVNNAGISGMFL-----ETESVERFRVVDINLTGVI 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 VIRLVAGENGQNEPDGQGGVYIINTASVAAFEQGVQQAAYSASKGIVGMLPLIARDIA 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 GKMTVIPAM---KDAQG--GSIVNISAAGLMLTSSYGASKGVGSLKLAVALG 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 PIGIRMTIAPGLFGPLL--TSLPEKANFLASQVFPFRLG--DPAEVAHYQALIE-- 242
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 172 TDRIRVNSVHPGFTYPTMRETGIRGEGEY--PNTPM--GRVNGEGLAGAVKILSDT 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 243 NPLNGEVIRLDG 255
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 229 SSYVTGAEIADVG 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-08-440-856A-4
Sequence 4, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
```

```

ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 809
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-4

Query Match      23.0% Score 300.5; DB 1; Length 333;
Best Local Similarity 32.5% Pred. No. 5.2e-25;
Matches 92; Conservative 46; Mismatches 106; Indels 39; Gaps 5;

QY 6 RSYKGLVAVITGASGGLTAERLVGOGASAVLLDLPNSGGEQAOKKLGNNCFAPADV 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 50 KRLGKVAIVTGARGGLAEARQAVAGARVVLADVLDEGATFARLGPARYOHLDTVI 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 66 TSEKDVQALALAKGKEQDVAVANCAGIYASKTYNLKKGQHTLEDFQVLDVNLMTFN 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 110 SVEEDVERAVRAVARGRDLVLCNNAGV--LGRQTRAKKILSEFDAGEFPRVIRVNALGA 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 126 FNVIRLVAGENGQNEPDGQGGVYIINTASVAAFEQGVQQAAYSASKGIVGMLPLIARDIA 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 ALGKHAHALAATQ-----RAGSIIYASVAGTGLGSHATASHALVGLTKNACE 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 LAPIGIRMTIAPGLFGPLL-----TSLP-----EKVA 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 223 LGANGIRVNCISPGVATPMLINAMRQGHDASTDADADIDIDIAVPSQVEYKMEVV 282
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 215 NPLASQVFPFRLGDPAEVAHYQALIEENPLNGEVIRLDGAI 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 283 RGLATLKGATLPRDIAE--AALFLASDSRSLTSGHNLVLDGAV 324
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-134-001C-4512
Sequence 4512, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4512
LENGTH: 263
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4512
```


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us-09-931-186-20.ra1

Page 5

Query Match 22.9%; Score 298; DB 4; Length 263;

Best Local Similarity 32.3%; Pred. No. 6.8e-25;

Matches 85; Conservative 43; Mismatches 107; Indels 28; Gaps 6;

12 VAVITGGASGIGLTAERLYGQASAVLLDLPNSGGEAQAQKL---GNCCVAPADVTSE 68
11 VAVITGGAAGIGLTAERLYGQASAVLLDLPNSGGEAQAQKL---GNCCVAPADVTSE 70
69 KDQVATLALAKGKGRVDVAVNCAGIAVASTYLNKKQGTHTLDFQRLVDVNLGTFNV 128
71 DQVSVLNQVVEHGGDLVNLVNNAGLGMPI-----ESVTPQEQVGVNVGVGFWG 124
129 IRLVAGEGONEPDGQGVYIINTASVAFEGQVQAASASKSGIYMTLPITARDLAP 188
125 IQAIEQF-----DLGSGKTIINTSQAQVGNAGLSYSTKFAVRGLTVQVARDLAE 179
189 IGIRVMTAPGLFGTPLLTLSPKVA-----NFLASQVPPFSRLGDPDAEYAHLY 237
180 KNITVNAFAPGIVETPMKKGIAEKLAENQPMEMWKOFTDQIAL-KRLSKPEDVANVY 238
238 QAIT--ENPFLNGEYIRLDGAIR 258
239 SFLASDSYITGOTIITVDGGR 261

RESULT 9

US-09-363-189B-6

Sequence 6, Application US/09363189B

Patent No. 6242228

GENERAL INFORMATION:

APPLICANT: SUGIYAMA, MASAKAZU

APPLICANT: TONOCHE, NAOTO

APPLICANT: SUZUKI, SHUNICHI

APPLICANT: YOKOZAKI, KENZO

TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF

FILE REFERENCE: 0010-1024-0

CURRENT APPLICATION NUMBER: US/09/363,189B

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1998-07-30

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.0

SEQ ID NO 6

LENGTH: 262

TYPE: PRN

ORGANISM: Glucobacter oxydans

US-09-363-189B-6

Query Match 22.7%; Score 296.5; DB 4; Length 262;

Best Local Similarity 32.0%; Pred. No. 9.9e-25;

Matches 87; Conservative 41; Mismatches 109; Indels 35; Gaps 7;

6 RSVKGLVAVITGGASGIGLTAERLYGQASAVLLDLPNSG---GQAQKTIQNNCVFAP 62
3 KKEGKVCIVTGGAGNIGLTAERLYGQASAVLLDLPNSG---GQAQKTIQNNCVFAP 62
63 ADVTSEKDVQATLALAKGKGRVDVAVNCAGIAVASTYLNKKQGTHTLDFQRLVDVNL 122
63 CDVTSEKDVQATLALAKGKGRVDVAVNCAGIAVASTYLNKKQGTHTLDFQRLVDVNL 117
123 MGTFTNIRLVAGEM-GQNEPDQGGQGVYIINTASVAFEGQVQAASASKSGIYMTLP 181
118 TGAHVHAKVAVSRQMTN-----YGRIVNTASMAQVGPNNKAAVAGSKALIALTET 170
182 IARLAPIGIRVMTAPGLFGTPLLTLSPKVA-----NFLASQVPPFSRLGDPDAEYAHLY 235
171 AADLAPYNTIRVNAISGQVGPMMERQVELAKVQSQFSTPKVVAQOMIGSVPM-R 229
226 RLSDPAEYAHLYQAII--ENPFLNGEYIRLDG 255
230 RYGDINEIPGVAVFLDGDSSFTMGVNLPIAG 261

RESULT 10

US-08-793-035-9

Sequence 9, Application US/08793035

Patent No. 6011201

GENERAL INFORMATION:

APPLICANT: Sladas, Antoni R.

APPLICANT: White, Andrew

APPLICANT: Chase, Dianne

APPLICANT: Elborough, Keiran

APPLICANT: Fentem, Phillip A.

TITLE OF INVENTION: B-ketoadcyl ACP Reductase Genes From

TITLE OF INVENTION: Brassica Napus

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: US

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,035

FILING DATE: 28-JUL-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9414622.2

FILING DATE: 20-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB95/01678

FILING DATE: 17-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kammerer, Patricia A.

REGISTRATION NUMBER: 29,775

REFERENCE/DOCKET NUMBER: MOBT-132

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713.787.1400

TELEFAX: 713.787.1440

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 315 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

US-08-793-035-9

Query Match 22.5%; Score 294; DB 3; Length 315;

Best Local Similarity 30.5%; Pred. No. 2.5e-24;

Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

4 ACSRYKGVAVITGGASGIGLTAERLYGQASAVLLDLPNSGGEA-----QAKKTIQNNC 58
66 AVPKYVESPVVVTGASRGKRIALSL-CKACKTVLVYARAKAEVYSQIEAVGGQA 124
59 VEPADVTEKDVQATLALAKGKGRVDVAVNCAGIAVASTYLNKKQGTHTLDFQRLVDVNL 118
125 ITFGGVSKAEADVEMAKTAIDAWGTIDVVVNNAGITRDTLLIRKKSQ-----WDEVI 178
119 DVNLMTGTEVITLVAGEGQNEPDGQGVYIINTASVAFEGQVQAASASKSGIYGM 178
179 DLNLGVFLCTQATKIKMK-----KGRITINIASVGLIGNIGNANTAAKAGVIGF 232
179 TLPIARDLAPIGIRVMTAPGLFGTPLLTLSPKVA-----NFLASQVPPFSRLGDPDAEYAHLY 238
233 SKTAREGASRNINNVVCPGFIASDMETAKLGEDMEKKILGTIPL-GRYGQEDVAVGIVE 291
239 AITENP---FNGEYIRLDGAI 257
292 FLALSPAASYITGQAFITDGI 313

RESULT 11
US-08-793-035-10
Sequence 10, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Slabas, Antoni R.
APPLICANT: White, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Elborough, Kelvin
APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-ketocyl ACP Reductase Genes From
TITLE OF INVENTION: Brassica Napus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
CLASSIFICATION: 880
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT-132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-793-035-10

Query Match 22.5%; Score 294; DB 3; Length 315;
Best Local Similarity 30.5%; Pred. No. 2.5e-24;
Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

DB 4 ACRSVGLVAVITGASGLATLAEPLVVGASAVLLDIPNSGGEA-----QAKLGNCC 58
DB 66 AVKVESPVVYVVGASRGISKAIALSL-GKAGCKVLVYARSAKEEVSKEIDVAVGQA 124
DB 59 VFAPADVTSEKDVOTLALAKGKFGVDVAVNCAIVASKTNNKKGQTHLEDFQRL 118
DB 125 ITFGGVSKADVDEAMKKTALIDAMGTIDVAVNAGITRDLIRKSKQ-----WDEVI 178
DB 119 DVNLMTGFNIRLVAGMGQNEPDGQGVIIINTASVAFEGQVQAAYSASRGIVM 178
DB 179 DNLVTGFLTQATKIMKK-----BKGRITINISVGLIGNIQANVAAKAGVIGF 232
DB 179 TLPIARDLAPIGIRVMTIAPGLCTPLTSLPERKANFLASQVPPFSRLGPAEVAHLYQ 238
DB 233 SKTAARAGASRNINNVVCPGFIASDTAKLGEDMKKITGITPL-GRYQAPDVAGLVE 291
DB 239 AIIENP---FLNGEVIRLDGAI 257

DB 292 FLATSPASVITGQAFITDGGI 313

RESULT 12
US-08-375-962B-13
Sequence 13, Application US/08375962B
Patent No. 5731195
GENERAL INFORMATION:
APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
APPLICANT: CHRISTER, ERIKSSON, ULF.
TITLE OF INVENTION: Isolated Nucleic Acid Molecule
TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,
TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,962B
FILING DATE: 20-January-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 6-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3864
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]
NAME/KEY: reductase (FABG)
US-08-375-962B-13

Query Match 22.0%; Score 287.5; DB 1; Length 244;
Best Local Similarity 29.6%; Pred. No. 8.8e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

DB 9 KGLVAVITGASGLATLAEPLVVGASAVLLDIPNSGGEQAKLGNCCVFAPADVTSE 68
DB 4 EKKILVVGASRGISRAETLAAARGGVITATSENQAQISIDLAGNGKGLMLNVTDP 63
DB 69 KDVOITALANGKRGFRVAVNCAIVASKTNNKKGQTHLEDFQRLDVNLMTGFN 128
DB 64 ASISEVLKIRAREBEVDIIYNNAGITRDLIRKSKQ-----EEMNDIIEFTNLSVFR 117
DB 129 IRLVAGMGQNEPDGQGVIIINTASVAFEGQVQAAYSASRGIVMTLPIARDLAP 188
DB 118 SKAVRAAMKK-----RHGRITITIGSVGTMGNGQANVAAAGLIGFSKSLAREVAS 171
DB 168 IGIKMTIAPGLFGPPLTSLPERKANFLASQVPPFSRLGPAEVAHLYQ--AIIENPFL 246
DB 172 KGIIVNVAPEFIETDMTRALSDORAGIQAQV-AGRLGAGQELIANNVATLADDEAYI 230

QY 189 IGRVMTIAPGLFETPLTSLPEKYNFLASQVFPFSPRLGDPAEVHAHQ--ATTENPFL 246
DB 172 RGIIVNVVAVPFIETDTRALSDQAGILAQVP-AGRLGGAQEIANAVAFASDEAAVYI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLHVNGGMV 243

RESULT 15
US-08-937-993-13
Sequence 13, Application US/08937993
Patent No. 6399344
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf; Simon, Andreas; Romert, Anna
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993
FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6399344ember-1995
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-937-993-13

Query Match 22.0%; Score 287.5; DB 4; Length 244;
Best Local Similarity 29.8%; Pred. No. 8.8e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGASGLGATARLVGOGASAVLLDPPSGGGAOKKIGNKVFAPADVTS 68
DB 4 EGKIAVTVGASRGISGRIATETLLARGGKVGITSTSEGAQALSDYLGANGKGLMNVTD 63
QY 69 KDVOTALALAKGFRGVAVVNCAGIIVASKIYNLKKGQTHLEDFQRYLDVNIKGTFFV 128

DB 64 ASIESVLEKIRAEFGEVDILVNNAGITRDNLIMRMD-----EEMNDIETNLSVERL 117
QY 129 IRLVAGEMGONEPDGCGGVIIINTASVAEFEGQCAAYASAKGIYGMTLPIARDLAP 188
DB 118 SKAVMRAMMK-----RGRITITGVSVTGTMKNGQANVAAKAGLIFSPSLAREVAS 171
QY 189 IGRVMTIAPGLFETPLTSLPEKYNFLASQVFPFSPRLGDPAEVHAHQ--ATTENPFL 246
DB 172 RGIIVNVVAVPFIETDTRALSDQAGILAQVP-AGRLGGAQEIANAVAFASDEAAVYI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLHVNGGMV 243

RESULT 16
5229279-7
Patent No. 5229279
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
BIOPOLYMERS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/556,535
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 67,695
FILING DATE: 29-AUG-1987
SEQ ID NO: 7
LENGTH: 246
5229279-7

Query Match 22.0%; Score 287.5; DB 6; Length 246;
Best Local Similarity 31.9%; Pred. No. 8.8e-24;
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY 12 VAVITGGASGLGATARLVGOGASAVLLDPPSGGGE---AQAKKIGNKVFAPADVTS 67
DB 5 IAYTGGGIGGIGTALICQRLAKDGRVAVAGCGPNSPREKMLEQOKALGFDFIASGNAVAD 64
QY 68 EKDVOITALALAKGFRGVAVVNCAGIIVASKIYNLKKGQTHLEDFQRYLDVNIKGTFFV 127
DB 65 WDKRTAFDKYKSEVGEDVLIINAGI---TRDYVERK---MTRADMDAVIDINLSLEFN 118
QY 128 VIRLVAGEMGONEPDGCGGVIIINTASVAEFEGQCAAYASAKGIYGMTLPIARDLAP 187
DB 119 VTKQVIDGMA---DRGM--GRIVNISVNGKQCFQOTVNSTKAGLHGFMAAQEVA 172
QY 188 IGRVMTIAPGLFETPLTSLPEKYNFLASQVFPFSPRLGDPAEVHAHQ--ATTENPFL 245
DB 173 RGIIVNVVAVPFIETDTRALSDQAGILAQVP-AGRLGGAQEIANAVAFASDEAAVYI 230
QY 246 NGEVIRLDGAIRM 259
DB 232 STGADFSINGGLHM 245

RESULT 17
5512669-4
Patent No. 5512669
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
REDUCTASE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 29-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535

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Page 9

FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 67,695
FILING DATE: 29-JUN-1987
SEQ ID NO: 4
LENGTH: 273
5512669-4

Query Match 21.7%; Score 282.5; DB 6; Length 273;
Best Local Similarity 31.5%; Pred. No. 3.8e-23;
Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

12 VAVITGASGIGLATAELVGGASAVLLDLPNSGGEAOAKLGNVCFA-----63
13 VAVITGASGIGLATAELVGGASAVLLDLPNSGGEAOAKLGNVCFA-----63
14 VALVTGSGRGIG-----AAISILKKAAGKVAASVAGNDAAKPKAENGIAV 51
15 ---DYTESEKDVQFALALAKGKFRVDVAVNCAAGIAVASTYNNKKGQTH--TLEDFOFVLT 118
16 4 YKMDVSSYEACVEGIAVEADLPIDLVNNAGIT-----KDMFKMTPDQNNAVI 103
17 DB 52 YKMDVSSYEACVEGIAVEADLPIDLVNNAGIT-----KDMFKMTPDQNNAVI 103
18 QY 119 DVNLKGTFFNVI-----FLV-----AGEGQ-NEPDGGQR---GVIIIN 152
19 DB 104 NTNLGTGFNTHPYWSGMRDRSFRGRIYNNISINGCKGOMQANYSWSGMRDRSFRGRIYV 163
20 QY 153 TASYAFAFGGGOAAYASASKGIGYGMTLPARDLAPIGIRVMTIAPGLGTPLTSLPEK 212
21 DB 164 ISSINGCKGOMQANYSWSGMRDRSFRGRIYNNISINGCKGOMQANYSWSGMRDRSFRGRIYV 223
22 QY 213 VAN-FLASOVFPRSLDPAEVAHLV--QAIENPLNGEVIPLDG 255
23 DB 224 VLNERIIPQIPV-GRLEGPDEIARIYVFLASDEAGFILTGSISANG 268

RESULT 18

US-09-134-001C-4431
Sequence 4431, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4431
LENGTH: 274
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4431

Query Match 21.5%; Score 280.5; DB 4; Length 274;
Best Local Similarity 31.7%; Pred. No. 6.3e-23;
Matches 85; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

12 VAVITGASGIGLATAELVGGASAVLLDLP-----NSGGEAOAKLGNVCFA 60
13 VAVITGASGIGLATAELVGGASAVLLDLP-----NSGGEAOAKLGNVCFA 60
14 IAVITGASTGIGASAVALLAEGAHVLLDISDLEFVOSINDNGKATAYV-----63
15 DB 10 IAVITGASTGIGASAVALLAEGAHVLLDISDLEFVOSINDNGKATAYV-----63
16 QY 61 APADYSEKDVQFALALAKGKFRVDVAVNCAAGIAVASTYNNKKGQTH--TLEDFOFVLT 118
17 DB 64 ---DISDKQYKQSEKIAQEFGHVDVFNNAAGVDNA-----GHIHEPYEVYDKIM 113
18 QY 119 DVNLKGTFFNVI-----FLV-----AGEGQ-NEPDGGQR---GVIIIN 152
19 DB 114 AVDMKGTPLVTKFLL-----PLMKRGGSIINTASFSGADLVYSSGNAKGGVAIN 166
20 QY 179 TPIARDLAPIGIRVMTIAPGLGTPLT-----TSLPEKANFLASQ--VPPFSRLGDPA 231
21 DB 167 TKSIAIEYGRNIRANALAPGTIEPLVDNLAGTSDEAGQTFENKQWVTPIGRLGTPD 226

232 EYAHVVO--AIENPLNGEVIPLDCAI 257
227 EVGRVAFVFLASDSSFTGETIRIDGV 254

RESULT 19

US-09-134-001C-4825
Sequence 4825, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4825
LENGTH: 249
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4825

Query Match 21.1%; Score 275.5; DB 4; Length 249;
Best Local Similarity 29.1%; Pred. No. 2e-22;
Matches 74; Conservative 54; Mismatches 105; Indels 21; Gaps 6;

13 AVITGASGIGLATAELVGGASAVLLDLPNSGGEAOA-----KLGNNVCFAADYVS 67
14 ALVTGASGIGLATAELVGGASAVLLDLPNSGGEAOA-----KLGNNVCFAADYVS 67
15 DB 10 ALVTGASGIGLATAELVGGASAVLLDLPNSGGEAOA-----KLGNNVCFAADYVS 67
16 QY 68 EKDQVOTALAKGKFRVDVAVNCAAGIAVASTYNNKKGQTH--TLEDFOFVLT 127
17 DB 69 GDEVKEMIKREVSGFSGVDVYNNAGITKNDLMPKME-----QEMDVVIDTNKGVEN 122
18 QY 128 VIRVAGMGNEPDGGQGVYIINTASVAFAGGOAAYASASKGIGYGMTLPARDL 187
19 DB 123 CIOQVTPQMKRQ-----KSGALINTSIVGAMNPGQAYVATKAGVIGLITARELA 176
20 QY 188 PIGIRVMTIAPGLGTPLTSLPEKANFLASQVPPFSRLGDPAEVAHLVQALLEN--PF 245
21 DB 177 SRGITVNAVADGFIYSQMTNALSDDLKDMLECIPL-KRGEEDTIANIVAFVFLASQKAY 235
22 QY 246 LMGVIRLDGAI 259
23 DB 236 ITGQTIHVNGATM 249

RESULT 20

US-09-238-481-2
Sequence 2, Application US/09238481
Patent No. 6110704
GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: FdG
FILE REFERENCE: GM10192
CURRENT APPLICATION NUMBER: US/09/238,481
CURRENT FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-238-481-2

Query Match 20.8%; Score 271.5; DB 3; Length 246;

Best Local Similarity 28.7%; Pred. No. 5.3e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY 13 AVITGASGLGATAEKLVGQASAVLLDLPNSGGEAQA-----KKGNNCFAPADYTS 67
DB 7 ALVTGASRGIGRSIALDLAEEGYN-VAVNVASKEKAEEVEIKAGVDSFALQANVAD 65
QY 68 EKDVOTALALAKGFGVADVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDVNLMTGN 127
DB 66 ADEKAMIKKEYVSQFGLDVLVNNAGITBDLTKRME-----QEMDDVIDTNLKGVEN 119
QY 128 VIRLVAGMGQNEPDGQGRVITNTASVAAFEGVQGAAYSASKGGIYGMPLPIARDLA 187
DB 120 CIQKAPQMLRQ-----RSGAIINTSSVGVAGVNPQGANVATKAGVIGLTKSARELA 173
QY 188 PIGIRVMTIAPGLGFTPLTSLPEKVFANFLASQVFPFSRLDPAEVAHLVQALLEN--PF 245
DB 174 SRGITVNAVAPGFIVSDMTDALSDLEKQMLTQPL-ARFGQDTDIANTVAFSLADKAKY 232
QY 246 LNGEVIRLDGAIRM 259
DB 233 ITGQTIHVNGGMYM 246

RESULT 21
US-09-572-810A-2
Sequence 2, Application US/09572810A
Patent No. 6365387
GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: Fabg
FILE REFERENCE: GM10192
CURRENT APPLICATION NUMBER: US/09/572, 810A
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 09/238, 481
PRIOR FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-572-810A-2

Query Match 20.8%; Score 271.5; DB 4; Length 246;
Best Local Similarity 28.7%; Pred. No. 5.3e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY 13 AVITGASGLGATAEKLVGQASAVLLDLPNSGGEAQA-----KKGNNCFAPADYTS 67
DB 7 ALVTGASRGIGRSIALDLAEEGYN-VAVNVASKEKAEEVEIKAGVDSFALQANVAD 65
QY 68 EKDVOTALALAKGFGVADVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDVNLMTGN 127
DB 66 ADEKAMIKKEYVSQFGLDVLVNNAGITBDLTKRME-----QEMDDVIDTNLKGVEN 119
QY 128 VIRLVAGMGQNEPDGQGRVITNTASVAAFEGVQGAAYSASKGGIYGMPLPIARDLA 187
DB 120 CIQKAPQMLRQ-----RSGAIINTSSVGVAGVNPQGANVATKAGVIGLTKSARELA 173
QY 188 PIGIRVMTIAPGLGFTPLTSLPEKVFANFLASQVFPFSRLDPAEVAHLVQALLEN--PF 245
DB 174 SRGITVNAVAPGFIVSDMTDALSDLEKQMLTQPL-ARFGQDTDIANTVAFSLADKAKY 232
QY 246 LNGEVIRLDGAIRM 259
DB 233 ITGQTIHVNGGMYM 246

RESULT 22
US-09-134-001C-4397
Sequence 4397, Application US/09134001C

Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCO
TITLE OF INVENTION: EPIDEMIOIDS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: CTC-007
CURRENT APPLICATION NUMBER: US/09/134, 001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055, 779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4397
LENGTH: 231
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4397

Query Match 20.6%; Score 269; DB 4; Length 231;
Best Local Similarity 33.3%; Pred. No. 9.1e-22;
Matches 66; Conservative 39; Mismatches 81; Indels 12; Gaps 2;

QY 8 VKGLVAVITGASGLGATAEKLVGQASAVLLDLPNSGGEAQAAGLNNCFAPADYTS 67
DB 5 VKERVAVVITGASGIGGALANKLSQOGASIVLGRNEQRINELVQQLNPAKVATADYTV 64
QY 68 EKDVOTALALAKGFGVADVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDVNLMTGN 127
DB 65 KSNIDMLKAVIDHFGIDVLVNSAGSLSKITD-----YVEQMDIMIDVNINGTLH 118
QY 128 VIRLVAGMGQNEPDGQGRVITNTASVAAFEGVQGAAYSASKGGIYGMPLPIARDLA 187
DB 119 VLQATLELYLKO-----SSGHILNTASVGFEPRTNAYGATKAAIHAIQTSLERELA 172
QY 188 PIGIRVMTIAPGLGFTPL 205
DB 173 RTGVKVISISPGKADTDM 190

RESULT 23
US-08-440-856A-3
Sequence 3, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440, 856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141

;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 337 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-440-856A-3

Query Match 20.6%; Score 268.5; DB 1; Length 337;
Best Local Similarity 30.9%; Pred. No. 1,9e-21;
Matches 88; Conservative 44; Mismatches 112; Indels 41; Gaps 6;

QY 6 RSVKGLAVITGASGLTARLVLGGASAVLLDLPNSGGEAOKKIGNNCFAPADY 65
DB 51 KRDKKAVITGGARGIGELIVLFAKHGRVVIADIDDAAGELASALGPQVSVRCDF 110
QY 66 TSEKDVOTALAKGKF-GRVDYAVNCAGIAVASKTYNLKKGQTHLEDFQRYLDVNLNG 124
DB 111 SEEDVRAVDMALSRHGRRLDYCNAGY-LGRQTRARSILSPAAEFDRVLRVNALG 169
QY 125 TENVIRLVAGEMGNEDDGGGQGVIIINTASVAFEGVQGAAYSAKSGIVGMLPIAR 184
DB 170 AALGMKHAARMAPR-----RGSIVSVASVAVLGGIGPAHYATSKHAIVGLTKNAC 223
QY 185 DLAPIGIRVMTIAPGLFGLPDL-----TSLP-----EK 212
DB 224 ELRHGVRVNCVSPFGVATPMLINAWRQHDATADADRDLDLDLVTVPSDQVEKME 283
QY 213 VANFLASQVPPPSRLGDPARYAHLVQAIINPFLNGEVITLDAI 257
DB 284 VVRGLATLKGPTLRPRDIAR-AVLFLASDEARYISGHNIYVDGV 327

RESULT 24

US-08-858-207A-270
Sequence 270; Application US/08858207A
Patent No. 6348328

;; GENERAL INFORMATION:
;; APPLICANT: Black, Michael
;; APPLICANT: Hodgson, John
;; APPLICANT: Knowles, David
;; APPLICANT: Nicholas, Richard
;; APPLICANT: Stodola, Robert
;; TITLE OF INVENTION: No. 6348328e1 Compounds
;; NUMBER OF SEQUENCES: 552
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Smithline Beecham Corporation
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406-0939
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/858, 207A
;; FILING DATE: 09-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/017670
;; FILING DATE: 14-MAY-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gimml, Edward R
;; REGISTRATION NUMBER: 38,891
;; REFERENCE/DOCKET NUMBER: P50475
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-4478
;; TELEFAX: 610-270-5090
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 270:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 186 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: NO. 6348328e
US-08-858-207A-270

Query Match 20.6%; Score 268; DB 4; Length 186;
Best Local Similarity 38.7%; Pred. No. 8.4e-22;
Matches 74; Conservative 23; Mismatches 72; Indels 22; Gaps 5;

QY 15 ITGSSRGIGLAIARLVLGGASAVLLDLPNSGGE-----AOAKKIGNNCFAPADYSE 68
DB 10 ITGSSRGIGLAIARLVLGGASAVLLDLPNSGGE-----NSGALSEELAEFSYGIKVPISGVSDF 65
QY 69 KDVOTALAKGKFRVDYAVNCAGIAVASKTYNLKKGQTHLEDFQRYLDVNLNGTFNV 128
DB 66 ADKRMIDDAIELSGSVLVNNAIGI--TODTIMIKM-----TEADFEKVLKYNLTGAENM 119
QY 129 IRLVAGEMGNEDDGGGQGVIIINTASVAFEGVQGAAYSAKSGIVGMLPIARLAP 188
DB 120 TOSVL-----KPMKARAGALITNMSVYGLMGNIGQANYASAKGILGFTKSVAREVAS 173
QY 189 IGRVMTIAPG 199
DB 174 RNIIRVVIAPG 184

RESULT 25

US-09-504-358-14
Sequence 14; Application US/09504358
Patent No. 6365376

;; GENERAL INFORMATION:
;; APPLICANT: Rouviere, Pierre E
;; APPLICANT: Brzostowicz, Patricia C
;; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEL
;; FILE REFERENCE: BCI001 US NA
;; CURRENT APPLICATION NUMBER: US/09/504,358
;; CURRENT FILING DATE: 2000-02-15
;; EARLIER APPLICATION NUMBER: 60/120,702
;; EARLIER FILING DATE: 1999-February-19
;; NUMBER OF SEQ ID NOS: 49
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 14
;; LENGTH: 256
;; TYPE: PRT
;; ORGANISM: Brevibacterium sp HCU
US-09-504-358-14

Query Match 20.5%; Score 267; DB 4; Length 256;
Best Local Similarity 30.9%; Pred. No. 1.8e-21;
Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;

QY 10 GLVAVITGASGLTARLVLGGASAVLLDLPNSGGEAOKKIGNNCFAPADY 66
DB 6 GKVAVITGAGAGRIQSELVASEGQVAVVVDNEGSRATDAIRASGVANVYKLDVS 65
QY 67 SEKDVOTALAKGKFRVDYAVNCAGIAVASKTYNLKKGQTHLEDFQRYLDVNLNG 124
DB 66 DESEVEIVVSDIKRRGAINVLYNNGVGAOK-----PHEIDERLDLVLSVDVG 118
QY 125 TENVIRLVAGEMGNEDDGGGQGVIIINTASVAFEGVQGAAYSAKSGIVGMLPIAR 184
DB 119 VEFMTKHCIYFQ-----AGS--GALVNFASIVIGVSGDELPIYHAKKAVVALLTQDAV 172
QY 185 DLAPIGIRVMTIAPGLFGLPDLTSLPEK-----VANFLASQVPPPSRLGDPARY--AH 235
DB 173 TYGPSNIRVNAVAPGILPLVYKELSRGPDGDGXTKLGMKAHPL-GRVGPPEEVAAT 231
QY 236 LVQAIINPFLNGEVITLDAIRMQ 260
DB 232 LPTLASEBASITGAVLPVDOGTYAQ 256

Thu Jun 26 06:55:04 2003

us-09-931-186-20.rtf

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Search completed: June 23, 2003, 14:35:43
Job time : 13.1667 secs

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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds
(without alignments)
1698.262 Million cell updates/sec

Title: US-09-931-186-23
Perfect score: 1304
Sequence: 1 MAACRSVKGLVAVITGGAS.....ENPFLNGEYIRLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: SP archaea:***
2: SP bacteria:***
3: SP fungi:***
4: SP human:***
5: SP invertebrate:***
6: SP mammal:***
7: SP mhc:***
8: SP organelle:***
9: SP phage:***
10: SP plant:***
11: SP rodent:***
12: SP virus:***
13: SP vertebrate:***
14: SP unclassified:***
15: SP viirus:***
16: SP bacteriap:***
17: SP archaeap:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240.5	95.1	252	4	Q96hd5 homo sapien
2	1159	88.9	261	11	Q99n15 mus musculu
3	1155	88.6	261	11	Q9CY13 mus musculu
4	983	75.4	196	4	Q8TCV9 homo sapien
5	751	57.6	258	5	Q19102 caenorhabdi
6	722	53.4	255	16	Q910T0 pseudomonas
7	714	54.8	255	16	Q8TBS0 bruceella me
8	692.5	53.1	252	16	Q8XWE0 raietonia s
9	674.5	51.7	250	16	Q06544 mycobacteri
10	673	51.6	255	16	Q92YS1 rhizobium m
11	670	51.4	253	16	Q98hm4 rhizobium 1
12	654	50.2	255	2	Q9AHY1 pseudomonas
13	645	49.5	257	16	Q8UFI2 agrobacteri
14	609	46.7	126	11	Q9DCX5 mus musculu
15	602.5	46.2	264	5	Q8T2L7 dictyosteli
16	598	45.9	260	16	Q9ABU6 caulobacter
17	386	29.6	443	2	Q93SJ3 myxococcus
18	376.5	28.9	246	16	Q8XLH1 clostridium
19	358.5	27.5	244	16	Q99YD6 streptococ
20	354	27.1	252	16	Q9HW15 pseudomonas
21	345.5	26.5	249	16	Q97DA6 clostridium
22	340.5	26.1	247	16	Q8R9W0 thermoaer
23	337.5	25.9	251	16	Q8YV10 anabaena sp
24	336.5	25.8	246	16	Q9KA03 bacillus ha
25	335.5	25.7	297	3	Q42774 neurospora
26	331	25.4	246	16	Q9K636 bacillus ha
27	329.5	25.3	248	2	Q9KJF1 thauera aro
28	328.5	25.2	243	16	Q9FBC3 streptococ
29	327.5	25.1	243	16	Q9CHF7 lactococcus
30	325.5	25.0	260	16	Q88068 streptomyc
31	325	24.9	262	2	Q919F8 streptomyc
32	322.5	24.8	271	10	Q94G09 cucumis sat
33	322.5	24.7	260	4	Q96KK9 homo sapien
34	321	24.6	261	13	Q8TUM4 oryzias lat
35	321	24.6	263	16	Q9KYM4 streptomyc
36	320	24.5	271	10	Q94G10 cucumis sat
37	319	24.5	258	2	Q9EPV0 streptomyc
38	317.5	24.3	246	2	Q9EX74 rhodococcus
39	317.5	24.3	261	6	Q8WKM4 macaca mula
40	317.5	24.3	259	16	Q8U616 agrobacteri
41	316.5	24.3	299	17	Q97UK6 sulfolobus
42	316	24.2	249	2	Q9AJT2 thauera aro
43	314.5	24.1	313	2	Q93HC0 streptomyc
44	313.5	24.0	247	16	Q9PFI6 xyella fas
45	313	24.0	247	16	Q8YD94 bruceella me
46	312.5	24.0	262	16	Q8YD94 pyrococcus
47	312.5	24.0	240	17	Q90Y54 pyrococcus
48	312	23.9	237	16	Q9AUX6 caulobacter
49	311.5	23.9	244	16	Q8WTW8 homo sapien
50	311.5	23.9	247	16	Q8ZFT5 yersinia pe
51	310.5	23.8	260	17	Q8U3B3 pyrococcus
52	310	23.8	267	10	P93697 vigna ungu
53	309	23.7	256	16	Q8ZB06 agrobacteri
54	308	23.6	253	16	Q8U759 agrobacteri
55	306.5	23.5	247	16	Q8U759 listeria mo
56	304.5	23.4	247	16	Q92AK1 listeria in
57	304	23.3	273	2	Q9F5J1 streptomyc
58	303.5	23.3	236	11	Q91VT4 mus musculu
59	302.5	23.2	247	2	Q9ZFP3 bacillus me
60	302	23.2	249	2	Q9LBS5 agrobacteri
61	302	23.2	248	16	Q8U9B5 agrobacteri
62	302	23.2	250	2	Q56840 xanthobacte
63	300	23.0	252	17	Q97U44 sulfolobus
64	299.5	23.0	256	5	Q9XZ28 caenorhabdi
65	297.5	22.8	254	16	Q92PP8 rhizobium m
66	297.5	22.8	258	16	Q33339 mycobacteri
67	297.5	22.8	538	2	Q8VM75 rhizobium s
68	296	22.7	245	16	Q8YD11 bruceella me
69	296	22.7	255	17	Q9H041 halobacteri
70	296	22.7	258	16	Q930L5 rhizobium m
71	295	22.6	260	16	Q9FBI1 streptomyc
72	295	22.6	315	10	Q949M3 brassica na
73	295	22.6	320	10	Q93X62 brassica na
74	294.5	22.6	267	2	Q91BG2 leifsonia a
75	294	22.5	265	16	Q9S2E4 streptomyc
76	294	22.5	328	10	Q93K67 brassica na
77	293	22.5	255	16	Q8RDG3 thermoaer
78	293	22.5	272	16	Q8YD11 bruceella me
79	292.5	22.4	405	16	Q98AS0 rhizobium 1
80	292	22.4	246	2	Q98AS0 streptomyc
81	291.5	22.4	270	4	Q93H33 streptomyc
82	290.5	22.3	254	4	Q93H33 homo sapien
83	290.5	22.3	254	10	Q949M2 brassica na
84	290.5	22.3	303	10	Q9BFX1 arabidopsis
85	289.5	22.2	245	16	Q9SCU0 thermoaer
86	288.5	22.1	244	16	Q8RDH9 escherichia
87	288.5	22.1	254	16	Q9RT26 delnocooccus
88	287.5	22.0	256	17	Q8T1T5 methanocarc
89	287	22.0	243	16	Q8RG25 fusobacteri

90 287 22.0 252 16 092pp0 092pp0 rhizobium m
91 286.5 22.0 246 2 09pf59 09pf59 streptomyce
92 286.5 22.0 247 2 0930p0 0930p0 azotobacter
93 286 21.9 275 16 09k4h0 09k4h0 streptomyce
94 285.5 21.9 317 10 093x68 093x68 brassica na
95 285.5 21.9 246 2 09R880 09R880 burkholderi
96 285.5 21.9 257 16 09WYD3 09WYD3 thermotoga
97 285.5 21.9 272 16 099RG1 099RG1 staphylococ
98 285 21.8 255 16 09pc02 09pc02 xyliella fas
99 284.5 21.8 248 2 09CH41 09CH41 lactococcus
100 283.5 21.7 253 16 08VDF2 08VDF2 azoarcus ev

ALIGNMENTS

RESULT 1
096HDS PRELIMINARY; PRT; 252 AA.
ID 096HDS
AC 096HDS;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Similar to hydroxacyl-coenzyme A dehydrogenase, type II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; BC008708; AA08708.1; -.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KM Oxidoreductase.
SQ SEQUENCE 252 AA; 25984 MW; F36BB71070CE872D CRC64;

Query Match 95.1%; Score 1240.5; DB 4; Length 252;
Best Local Similarity 96.2%; Pred. No. 4.4e-78;
Matches 251; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 MAAACRSYKGLVAVITGGASGLGATAEELVGGASAVLDDLPNSGGEAQAQKLGNNCYF 60
DB 1 MAAACRSYKGLVAVITGGASGLGATAEELVGGASAVLDDLPNSGGEAQAQKLGNNCYF 60
QY 61 APADVTSEKDVQATLALAKGKFGKRDVAVNCAGIAVASKTYNLRKGGTHLEDFORVLDV 120
DB 61 APADVTSEKDVQATLALAKGKFGKRDVAVNCAGIAVASKTYNLRKGGTHLEDFORVLDV 120
QY 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAAPFGVQAAYASASKGIVGKTL 180
DB 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAAPFGVQAAYASASKGIVGKTL 180
QY 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAAPFGVQAAYASASKGIVGKTL 180
DB 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAAPFGVQAAYASASKGIVGKTL 180
QY 181 PIARDLAPGIRVMTIAPGLFGPILTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
DB 181 PIARDLAPGIRVMTIAPGLFGPILTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
QY 181 PIARDLAPGIRVMTIAPGLFGPILTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
DB 181 PIARDLAPGIRVMTIAPGLFGPILTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
DB 241 IENPFLNGEYIRLDGAIRMOP 261
QY 232 IENPFLNGEYIRLDGAIRMOP 252
DB 232 IENPFLNGEYIRLDGAIRMOP 252

RESULT 2
099N15 PRELIMINARY; PRT; 261 AA.
ID 099N15
AC 099N15;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Short chain L-3-hydroxacyl-CoA dehydrogenase.
GN HSD17B10 OR SCHAD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21095701; PubMed=1165016;
RA He X.Y., Kertz G., Chu C.H., Lin D., Yang Y.Z., Menta P., Schulz H.,
RA Yang S.Y.;
RA "Molecular cloning, modeling, and localization of rat type 10 17beta-
RT hydroxysteroid dehydrogenase.";
RL Mol. Cell. Endocrinol. 171:89-98(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AF233683; AKI15008.1; -.
DR HSSP; 070351; 1E6W.
DR MGD; MGI:133871; Hsd17b10.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Oxidoreductase.
SQ SEQUENCE 261 AA; 27273 MW; F371ED8A15FCFAF CRC64;

Query Match 88.9%; Score 1159; DB 11; Length 261;
Best Local Similarity 87.7%; Pred. No. 1.9e-72;
Matches 229; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLVAVITGGASGLGATAEELVGGASAVLDDLPNSGGEAQAQKLGNNCYF 60
DB 1 MAAACRSYKGLVAVITGGASGLGATAEELVGGASAVLDDLPNSGGEAQAQKLGNNCYF 60
QY 61 APADVTSEKDVQATLALAKGKFGKRDVAVNCAGIAVASKTYNLRKGGTHLEDFORVLDV 120
DB 61 APADVTSEKDVQATLALAKGKFGKRDVAVNCAGIAVASKTYNLRKGGTHLEDFORVLDV 120
QY 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAAPFGVQAAYASASKGIVGKTL 180
DB 121 NLMTGFNVIRLVAGEMGNEPDGGGGRVITNTASVAAPFGVQAAYASASKGIVGKTL 180
QY 181 PIARDLAPGIRVMTIAPGLFGPILTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
DB 181 PIARDLAPGIRVMTIAPGLFGPILTSLPEKVSNTLASQVFPSPRLGDPAYAHLYQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
DB 241 IENPFLNGEYIRLDGAIRMOP 261

RESULT 3
09CCT3 PRELIMINARY; PRT; 261 AA.
ID 09CCT3
AC 09CCT3;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hydroxacyl-coenzyme A dehydrogenase, type II.
GN HSD17B10 OR HADH2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kondo H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamagata T.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kariya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hasehira Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 CL Nature 409:685-690(2001),
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL: AK013340; BAB28800.1; -.
 DR HSSP: 070351; 1E6W.
 DR MGD: MGI:1333871; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 261 AA; 27273 MW; F36CD179C7FCEFAF CRC64;

Query Match 88.6%; Score 1155; DB 11; Length 261;
 Best Local Similarity 87.4%; Pred. No. 3.6e-72;
 Matches 228; Conservative 19; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MAACRSYGLAVITGASGLATAEPLVVGASAVLLDPNSGGEAQAQKLNCCVF 60
 DB 1 MAASVRSYGLAVITGASGLATAEPLVVGASAVLLDPNSGGEAQAQKLNCCVF 60
 QY 61 AAPADVTSEKDVOTALALAKGKFRVAVNACAGIAVASKTYNKKQOTLIDFQVLDV 120
 DB 61 AAPADVTSEKDVOTALALAKGKFRVAVNACAGIAVASKTYNKKQOTLIDFQVLDV 120
 QY 121 NLMGTENVIRLVAGENGONPDGQGRGVINTASVAEFGQGAAYASAKGIVGML 180
 DB 121 NLMGTENVIRLVAGENGONPDGQGRGVINTASVAEFGQGAAYASAKGIVGML 180
 QY 181 PIARDLAPGIRVMTIAPGLFGTPLLTLSPKYSNLAQVPPPSLGPAPFAHLYQAI 240
 DB 181 PIARDLAPGIRVMTIAPGLFGTPLLTLSPKYSNLAQVPPPSLGPAPFAHLYQAI 240
 QY 241 IENPFLNGEYIRLDGAIKMP 261
 DB 241 IENPFLNGEYIRLDGAIKMP 261

RESULT 4
 ID Q8TCV9 PRELIMINARY; PRT; 196 AA.
 AC Q8TCV9;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein
 DE (Fragment).
 GN ERAB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Deininger M.H., Meyermann R., Schluesener H.J.,
 RT "Expression, release and induction of endoplasmic reticulum-associated
 RT amyloid beta-binding protein in brain disease."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY092415; AAM18189.1; -.
 FT NON-TER 1
 FT NON-TER 196
 SQ SEQUENCE 196 AA; 20581 MW; 240DE149668AAGA CRC64;
 Query Match 75.4%; Score 983; DB 4; Length 196;
 Best Local Similarity 99.5%; Pred. No. 1.8e-60;
 Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 51 AKKIGNNCFVAPADVTSEKDVOTALALAKGKFRVAVNACAGIAVASKTYNKKQOTHT 110
 DB 1 AKKIGNNCFVAPADVTSEKDVOTALALAKGKFRVAVNACAGIAVASKTYNKKQOTHT 60
 QY 111 LEDFQRYLDVNLMTGFNVIRLVAGENGONPDGQGRGVINTASVAEFGQGAAYSA 170
 DB 61 LEDFQRYLDVNLMTGFNVIRLVAGENGONPDGQGRGVINTASVAEFGQGAAYSA 120
 QY 171 SKGIVGNTLPIDAPLPIGIRVMTIAPGLFGTPLLTLSPKYSNLAQVPPPSRLGDP 230
 DB 121 SKGIVGNTLPIDAPLPIGIRVMTIAPGLFGTPLLTLSPKYSNLAQVPPPSRLGDP 180
 QY 231 AEVAHLVQAITENPFL 246
 DB 181 AEVAHLVQAITENPFL 196

RESULT 5
 ID Q19102 PRELIMINARY; PRT; 258 AA.
 AC Q19102;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Probable 3-hydroxacyl-CoA dehydrogenase F01G4.2 type II (EC 1.1.1.35)
 DE (Type II HADH).
 GN F01G4.2.
 GN Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Caenorhabditis.
 OX NCBI_TaxID=6259;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris B.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-CoA + NAD(+) = 3-OXOACYL-CoA +
 CC NADH.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC FAMILY (SDR).
 DR EMBL: Z68341; CAA92764.1; -.
 DR HSSP: 070351; 1E6W.
 DR WormPep: F01G4.2; CE03127.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
 FT NP_BIND 11 36
 FT ACT_SITE 165 165
 FT SEQUENCE 258 AA; 27143 MW; 86BF2568EE692B3 CRC64;

Query Match 57.6%; Score 751; DB 5; Length 258;
 Best Local Similarity 59.9%; Pred. No. 2.5e-44;
 Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;
 QY 3 AACRSYGLAVITGASGLATAEPLVVGASAVLLDPNSGGEAQAQKLNCCVF 62
 DB 2 SALRSTKGLVAVITGASGLGKGAPEVLAKAGNVAIIDLPQSKADVAKEIGG--ITP 59
 QY 63 ADVTSKDVOTALALAKGKFRVAVNACAGIAVASKTYNKKQOTHTLEDQRYLDVNL 122
 DB 60 ASVTSEEEVRAFAFVQAEYGRDLAVNACAGIAVAFKLYSYQKKKHVDFEIRIQTIDVNV 119

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QY      123  MGFENVIRLVAGEMGNEPDGGRGVIINTASVAAPFEGVGOAAYSASKGIVGMLTPI 182
      :|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      120  LGTFNVRIRVALMGHEKDANGRGVINTASVAAPDGTGSAVSASKGALVGMTLPL 179
QY      183  ARDLAPIGIRVMTIAPGLFGTPLLTSPEKVSNEFASQVFPSPRLDPAEYAHLYOATIE 242
      :|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      180  ARDPAGGIGIRFNFTIAPGLMDTPLLSPLEKVSFLLQPLPNPRLGHPHEYALVQHIE 239
QY      243  NPELNGEVRILDGAIRM 259
      :|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      240  NQILNGETIRFDGALRM 256

RESULT 6
Q910T0 PRELIMINARY; PRT; 255 AA.
ID 0910T0
AC 0910T0;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA2554.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou K.,
  Gardner R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
  Brody L.L., Coulter S.N., Folger K.R., Kas A., Labig R., Lim R.M.,
  Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
  Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
  "Complete genome sequence of Pseudomonas aeruginosa PA01, an
  opportunistic pathogen."
RT Nature 406:959-964(2000).
RL Nature 406:959-964(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
  (SDR) FAMILY.
CC EMBL: AE004683; AGO5942.1; -
DR HSSP: O70351; 1E3S.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 255 AA; 26426 MW; EB8FF28712D2936D CRC64;

Query Match 55.4%; Score 722; DB 16; Length 255;
Best Local Similarity 57.5%; Pred. No. 2,5e-42;
Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;

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RESULT 7
Q8YBS0 PRELIMINARY; PRT; 255 AA.
ID 08YBS0
AC 08YBS0;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier protein) reductase (Ec 1.1.1.100).
GN BMEI10816.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapatal V., Redkar R.J., Patra G., Mujer C., Los T.,
  Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
  Jablonoski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
  Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
  Haselkorn R., Kyprides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
  Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL: AE009715; AAL54058.1; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 255 AA; 26263 MW; 5CF61D4B37F6B730 CRC64;

Query Match 54.8%; Score 714; DB 16; Length 255;
Best Local Similarity 57.1%; Pred. No. 8.8e-42;
Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

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Db 187 MTIAPGJFEETPMAGTEEVNARSLAAGVPPPPRLGRPOETAAARHIENSMLNGEVIRL 246
 QY 254 DGAIRM 259
 Db 247 DGAIRM 252

RESULT 13

ID Q8UF12 PRELIMINARY: PRT: 257 AA.
 AC Q8UF12;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II.
 GN ATU1415 OR AGR_C_2613.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,
 RA Chapman P., Cleenden J., Deatherage G., Gillet W., Grant C.,
 RA Kutayman T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Quicilo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houtrel K., Gordon J., Vaudin M., Doughty D., Scott C., Iappas C., Markelz B.,
 RA Woliam C., Allinger M., Doughty D., Scott C., Iappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cleo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL: AE009102; AAL42421.1;
 DR EMBL: AE008067; AAK67207.1;
 KW Complete Proteome.
 SQ SEQUENCE 257 AA: 26622 MW; FF74A61FFC4B2B5C CRC64;

Query Match 49.5%; Score 645; DB 16; Length 257;
 Best Local Similarity 51.7%; Pred. No. 5e-37;
 Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

QY 7 SYKGLVAVITGGASGLGATATRLVGGASAVLLDLPSSGGEAQAQKKNVCYAPADVT 66
 Db 2 NIEGAGALVTGASGLGAIVAVAMLAARGAATVITDRNGEAAKRLAAEIGRAV--QGVT 59
 QY 67 SEKDVOTALAKGKFGVADVAVNCAIGVAVASKTYNKKQTHLEDFQRLVDYINLMTF 126
 Db 60 SDADQAIAIKVAASAKGRLIRIVNCAIGTAGRI--LGRBPQPLGDEQYIRNLIGTF 117
 QY 127 NVIRIVAGEKGNEDDQ---GQRGVINTASVAAPFGVGOAAYSAKSGIYQMTLPI 182
 Db 118 NMMRLAAAHMEREDDEGDSRQDNGIVNTASVAAPFGVGOAAYSAKSGIYSLAP 177
 QY 183 AADLAPIGIRVITAPGTFPTLTLSPKVSNFLASOVPPSPRSGDAEVAHLVOAITE 242
 Db 178 ARELARIRIVNTAVAGTIFLPLDGLQFQVQESLAGIIPHSRLGDPARFADIVRFLIE 237

QY 243 NPFLNCEVIRLDGAIRMOP 261
 Db 238 NDYMNCEVIRLDGAIRMOP 256

RESULT 14

ID Q9DCX5 PRELIMINARY: PRT: 126 AA.
 AC Q9DCX5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hydroxyacyl-coenzyme A dehydrogenase, type II.
 GN HSD17B10 OR HADH2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Rietschman W., Gaasterland T., Glasl C., King B., Kochiwa H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyshaw-Solis A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC EMBL: AK002368; BAB22046.1; -;
 DR HSSP: O70351; 1E6W.
 DR MGD: MGI:133871; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 KW Oxidoreductase.
 SQ SEQUENCE 126 AA: 13265 MW; 78FEB6D441B9989D CRC64;

Query Match 46.7%; Score 609; DB 11; Length 126;
 Best Local Similarity 95.2%; Pred. No. 6.5e-35;
 Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 136 MGONPDQGGGRRGVIINTASVAAPFEGVGOAAYSAKSGIYQMTLPIARDLAPIGIRVMT 195
 Db 1 MGONPDQGGGRRGVIINTASVAAPFEGVGOAAYSAKSGIYQMTLPIARDLAPIGIRVMT 60
 QY 196 IAPLFTPLTSLPEKVSNFLASOVPPSPRSGDAEVAHLVOAITEPFLNCEVIRLDG 255
 Db 61 IAPLFTPLTSLPEKVSNFLASOVPPSPRSGDAEVAHLVOAITEPFLNCEVIRLDG 120
 QY 256 AIRMOP 261
 Db 121 AIRMOP 126
 RESULT 15
 Q8T2L7

Db 8 AVITGXXXRXRAGRPARRPRL---ARSALFDLNDKGAANAVALGADRRARFNNVNS 63
 Qy 67 SEKDVOFTALALAKGKFGKRDVAVNCAGIAVASKTYNLKKQGTHTLEDFORVLDVLMKTE 126
 Db 64 DEAAVTAIDQAHDLGGINAMNAGILGAGR--LKEGFMPLAGFGQVVMNLVGSF 121
 Qy 127 NVIRLVAGMGONPDQGGQGVYIINTASVAAFESQVQOAYASAKSGIVGKTLPIADL 186
 Db 122 NVAKAANRMCNHEAGTGERGVYIINTASIAVEGOIQOAAVYASAKGVSMTLPMAREL 181
 Qy 187 APGIRVMTIAPGLFTPLTSLPEKV 213
 Db 182 SRFGIRVNTIAPGVMTIAPVMDMPAV 208

RESULT 18

Q8XHL1 PRELIMINARY: PRT: 246 AA.

AC Q8XHL1
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-JUN-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 3-oxoacyl-(acyl-carrier-protein) reductase.
 GN FABG OR CPE1070.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 NC NCB1_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashta A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL: AP003189; BAB80776.1;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFamily.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Complete proteome.
 SQ SEQUENCE 246 AA; 26267 MW; CD90B8C650EC917 CRC64;

Query Match 28.9%; Score 376.5; DB 16; Length 246;
 Best Local Similarity 35.8%; Pred. No. 1.5e-18;
 Matches 93; Conservative 47; Mismatches 97; Indels 23; Gaps 7;

Qy 8 VKGLVAVITGASGLGATATERTLVGOGASAVLLDLPNSGGEAQAQKL-----GNNCVFP 62
 Db 2 LKQKVALVTGTRIGRAIALKLDAGAN-IVINRNSDKAEELKALIEKKGVKVLTK 60
 Qy 63 ADVTSEKDVOFTALALAKGKFGKRDVAVNCAGIAVASKTYNLKKQGTHTLEDFORVLDVNL 122
 Db 61 CDISNFDPSKNIMDKCEVFGKIDILVNNAGITKDLIMRKE-----EDFNVIDVNL 114
 Qy 123 MGTFNVIRLVAGMGONPDQGGQGVYIINTASVAAFESQVQOAYASAKSGIVGKTLPI 181
 Db 115 KGTFNCAKHAASAIMLK-----QRFKIIINMTSVGIIAGNAGOVNSASKACVIGLTKS 167
 Qy 182 IARLAPIGIRVMTIAPGLFTPLTSLPEKVSNFLASQVFPFRLGDDPAEVAHLVQAI 241
 Db 168 LAKLGSRGITVYNAVAAGFINTDMTASLSEKVEKESKNIP-L-KRLDPEDEVANLVQFLA 226
 Qy 242 ENP--FLNGEYIRLDGAIRM 259
 Db 227 SDANVITGVINVDGKVM 246

RESULT 19
 Q99YD6 PRELIMINARY: PRT: 244 AA.
 ID Q99YD6

AC Q99YD6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative beta-ketoacyl-ACP reductase (PC 1.1.1.100).
 GN FABG OR SPY1749.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NC NCB1_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / SEROTYPE M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Stvorov A.N., Kenton S., Lal H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
 RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC EMBL: AE006603; AAK34493.1; -
 DR HSPF: P50162; IAB1.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR01608; BACTINVASINC.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 DR OXidoreductase; Complete proteome.
 KW SEQUENCE 244 AA; 26002 MW; 67ECE23870D40D65 CRC64;

Query Match 27.5%; Score 358.5; DB 16; Length 244;
 Best Local Similarity 35.4%; Pred. No. 2.7e-17;
 Matches 92; Conservative 41; Mismatches 102; Indels 25; Gaps 5;

Qy 8 VKGLVAVITGASGLGATATERTLVGOGASAVLLDLPNSGGEAQAQKL-----GNNCVFP 60
 Db 3 IKGNIFITGSTRIGILAMAHQFASLEIANIVL-----NGRSALISELIVASPTDYGVTVT 57
 Qy 61 APADVTSEKDVOFTALALAKGKFGKRDVAVNCAGIAVASKTYNLKKQGTHTLEDFORVLDV 120
 Db 58 ISGDVSEASEAKRVNNEALIESIGSIDVLVNNAGIT-----NDKIMLKTDEDFERYLKI 111
 Qy 121 NMGTFNVIRLVAGMGONPDQGGQGVYIINTASVAAFESQVQOAYASAKSGIVGKTL 180
 Db 112 NLTGAFNNMGQSVL-----KPMIKAROGAIIIVSVGLTGIGICQANAAAKAGWIGTPT 165
 Qy 181 PIARLAPIGIRVMTIAPGLFTPLTSLPEKVSNFLASQVFPFRLGDDPAEVAHLVQAI 240
 Db 166 SVAREVAAARNICVNAIAPGFIESDMGVLPKMQSIIQLPM-KRIKAGDEVANLASF 224
 Qy 241 IENPFLNGEYIRLDGAIRM 260
 Db 225 VEDDYITGVINADGGMWQ 244

RESULT 20

Q9HW15 PRELIMINARY: PRT: 252 AA.

AC Q9HW15
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Probable short-chain dehydrogenase.
 GN PA4389.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subphylum; Pseudomonadaceae;
 OC Pseudomonas.
 NC NCB1_TaxID=287;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PA01:
 RX MEDLINE-20437337; PubMed-10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Gardner L.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Felder K.R., Kas A., Lardig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC EMBL: AE004854; AAC07777.1; -
 DR HSP: P50163; 2AE1.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001064; Cys_talln.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR Oxidoreductase; Complete proteome.
 KW SEQUENCE 252 AA; 26720 MW; F1F445AB2C2D8DE CRC64;
 Query Match 27.1%; Score 354; DB 16; Length 252;
 Best Local Similarity 35.1%; Pred. No. 5.6e-17;
 Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;
 QY 8 VKGLVAVITGASGLGATAEIRLVGOGASAVLLDLPN-----SGEAAQAKKLG 55
 DB 3 LKXKVIITGGCGGGRAMGEYLAGARLALVDLNRRLDEAVAAKAGADANA---- 58
 QY 56 NNCVFPADYTSKDVOTALAKKFGFRVDVAVNCAGIAVASKTYNLKKQTH--TLED 113
 DB 59 -----YVCNVADEEQYTHMVAAQVAFDGAINGLVNAGITRLDGLITIKVCGQLSKMSLQ 113
 QY 114 FQRLVDVNLGTFNVRFLVAVGEMQ--NEPDGCGGCGVITNTASVAFEGOVQAAYSAS 171
 DB 114 MGSVIDVNLGVLGFLCREVAKKMIELKNE-----GALVNISSISR-AGNMGQANYSAA 165
 QY 172 KSGIVMTLPIADLPAGIRVMTAPGLFGTPLTSLPEKYSNFLASQVPPSRIGDPA 231
 DB 166 KAGVADTYWMAKELRYGIRVAGVAPGFIETEMTGMPEALEKMTAGIPL-KRMGRFV 224
 QY 232 EVAHLVQATIEENPELNGEVIRLDGARM 259
 DB 225 EIAHSVAYIFENDYTRGVLELDGRL 252
 RESULT 21
 Q97DA6 PRELIMINARY; PRT; 249 AA.
 ID 097DA6
 AC 097DA6
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE 3-ketoacyl-acyl carrier protein reductase.
 GN CAC3574.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiales; Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE-21359325; PubMed-11466286;
 RA Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Oiu D., Hilti J., Wolf Y.I.,
 RA Tatusov R.L., Sabatini F.V., Smith D.R.,
 RA Bennett G.N., Koonin E.V., Smith D.R.,
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium *Clostridium acetobutylicum*."
 RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL: AE007854; AAX81497.1; -
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HLM_basic.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 249 AA; 26247 MW; B13DVEDAC21A626A CRC64;
 Query Match 26.5%; Score 345.5; DB 16; Length 249;
 Best Local Similarity 33.2%; Pred. No. 2.1e-16;
 Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;
 QY 8 VKGLVAVITGASGLGATAEIRLVGOGASAVLLDLPNSGGEAQ-----AKKLGNNCYFAP 62
 DB 5 LSGVAVVATGAGRGRLAALKAEANLV-VNRRSEAFQKLIKELIELSGKAVAK 63
 QY 63 ADVTSKDVOTALAKKFGFRVDVAVNCAGIAVASKTYNLKKQTHLTEDFQRYVDNL 122
 DB 64 ADISKYEAETIIKKALDEYGTDLVNNAGITDNLRLRKE-----EDFQSVINVL 117
 QY 123 MGFNVIRLVGEGGONEPDGCGVITNTASVAFEGOVQAAYSASGKGIYMTLP 182
 DB 118 KGAFNCIKHTSRVMLK-----KSGKITINSSVITGLGNAGVNNVAAKAGITGMKSV 171
 QY 183 ARDLAPIGIRVMTAPGLFGTPLTSLPEKYSNFLASQVPPSRIGDPAEYHLVQAIE 242
 DB 172 AKELASRIITVNAAPGIIKSDMTDALDKORESIVAVPL-NKVGAEADVANLVLELAS 230
 QY 243 --NPELNGEVIRLDGARM 259
 DB 231 DLSITIGQVITNDGGMV 249
 RESULT 22
 Q8R9W PRELIMINARY; PRT; 247 AA.
 ID 08R9W
 AC 08R9W
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Dehydrogenases with different specificities (related to short-chain
 DE alcohol dehydrogenases).
 GN FA83 OR TTE1472.
 OS Thermobacterium tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermobacteriales; Thermobacteriales; Thermobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MB47 / JCM11007;
 RX MEDLINE-213992816; PubMed-11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of *T. tengcongensis* genome."
 RL Genome Res. 12:689-700(2002).
 DR EMBL: AE013105; AAM24694.1; -
 KW Complete proteome.
 SQ SEQUENCE 247 AA; 26606 MW; 357D82B8C60E7947 CRC64;
 Query Match 26.1%; Score 340.5; DB 16; Length 247;
 Best Local Similarity 34.3%; Pred. No. 4.7e-16;
 Matches 87; Conservative 48; Mismatches 100; Indels 19; Gaps 6;
 QY 12 VAVITGASGLGATAEIRLVGOGASAVLLDLPN--SGEAA--QAKKLGNNCYFADYTS 67
 DB 7 VAFVITGSGIGIRALAVLANDGFIATTYKDKSABEYVEKKHVDALAKCDVSK 66
 QY 68 EKDVOITALAKKFGFRVDVAVNCAGIAVASKTYNLKKQTHLTEDFQRYVDNLGTFN 127
 DB 67 YHEVEKAVEKVEEFGSIDVYVNNAGITKMDLIKMEB-----EEMDQVIDVNLKGAFN 120

RA Buerger F., Broers B., Weiss H.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL: AF042860; AAB9799.1; -;
 DR EMBL: AL390092; CAB98248.1; -;
 DR HSSP: 070351; IE6W.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 297 AA; 31342 MW; 8DC08FEDF584196F CRC64;

Query Match

25.7%; Score 335.5; DB 3; Length 297;

Best Local Similarity 31.7%; Pred. No. 1,3e-15;
 Matches 97; Conservative 40; Mismatches 102; Indels 67; Gaps 8;

QY 6 RSYKGLVAVITGASGLGATAFRLVGGASAVLDLPNS-----GGEAQ 50
 DB 2 RSLHKOALITGGSGGLAARLYLEGCVTLGRTSTLORASQSLLSQPLHSPAQ 61
 QY 51 AKILGNVCVAPADVTSEKDVOTAL-ALAKGFGFVDVAVNCAGIAVAS--KTYNLKRG 106
 DB 62 QPSDTRKVSYPHPLNVSASWEDLLOSNGSGKGRVDILINCAGITQRSPLMKT----- 115
 QY 107 QHTLDEFORVLDVNIAGTFNVIIRLVAGENGQNEP-----DOG- 145
 DB 116 --SIEVEGLIDLTNLTGCKFVGRAMLRRNPQOHPRVRADEGAGVWEGTEEG 172
 QY 146 -----ORGVIINTASVAFAFEGOVGOAAYSASKGIYGMTLPIDRLAPIGI 191
 DB 173 KGGKGGVAREGVEQEGVILINVASLAKQCVIGTSYAAKAGVGLTSLAHEYGRSGI 232
 QY 192 RVMTIAPGLFGTPLLTLSPKVSNTLASQVPPPSRLGDPAEVAHLVQAITENPFLNGEVI 251
 DB 233 RVNAVYLPFGYIETIMTGLK---NPSILQCIPL-GRFGTDEVADALFLIKNPYANNCVL 288
 QY 252 RLDDGI 257
 DB 289 NLDDGL 294

Search completed: June 23, 2003, 14:32:49
 Job time : 32.6667 secs

Thu Jun 26 06:55:06 2003

us-09-931-186-23.rsp

Page 1

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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.83333 Seconds
(without alignments)
1381.956 Million cell updates/sec

Title: US-09-931-186-23

Perfect score: 1304

Sequence: 1 MAACRSVKGVLAVITNGAS.....ENPFLNGEVIRLDGARMPQ 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1299	99.6	261	1	HCD2_HUMAN
2	1208	92.6	261	1	HCD2_BOVIN
3	1153	88.4	260	1	HCD2_RAT
4	1134	87.0	261	1	HCD2_MOUSE
5	910	63.8	255	1	HCD2_DROME
6	382.5	29.3	247	1	YD50_MYCTU
7	343	26.3	246	1	FABG_THEMA
8	338	25.9	320	1	FABG_CUPLA
9	331.5	25.4	261	1	FABG_HUMAN
10	330.5	25.3	244	1	FABG_VIBCH
11	316.5	24.3	260	1	DHB8_MOUSE
12	312.5	24.0	246	1	FABG_BACSU
13	312.5	24.0	247	1	FAGI_SYNT3
14	305	23.4	260	1	YK02_MYCTU
15	304	23.3	255	1	YMPD_BACSU
16	302	23.2	255	1	2BHD_STREX
17	296.5	22.7	548	1	YAYI_RHISN
18	293.5	22.5	244	1	FABG_VIBHA
19	293.5	22.5	248	1	FABG_AQUAE
20	291.5	22.4	244	1	FABG_ECOLI
21	291	22.3	249	1	BAV1_EUBSP
22	287	22.0	263	1	UCPA_SALTY
23	286.5	22.0	246	1	FABG_ALCEU
24	285.5	21.9	244	1	FABG_SALTY
25	285.5	21.9	256	1	Y019_THEMA
26	285	21.9	248	1	PHAB_ACISS
27	283.5	21.7	246	1	NODG_AOBRP
28	283	21.7	259	1	CMTB_PSEPU
29	282.5	21.7	248	1	FABG_CHIMU
30	279	21.4	250	1	LINC_PSEPA
31	278.5	21.4	241	1	PHBB_ZOORA
32	277	21.2	246	1	PHBB_CHRVT
33	276.5	21.2	289	1	YHDF_BACSU

34	276	21.2	249	1	BA72_EUBSP
35	276	21.2	319	1	FABG_ARATH
36	275	21.1	263	1	UCPA_ECO57
37	275	21.0	263	1	UCPA_ECOLI
38	273.5	21.0	247	1	FABG_CHLTR
39	272.5	20.9	240	1	FAB2_SYNT3
40	271	20.8	250	1	LINC_PSEPA
41	271	20.8	251	1	Y325_THEMA
42	269.5	20.7	242	1	FABG_HAEIN
43	269.5	20.7	262	1	DHB8_BACSU
44	269.5	20.6	261	1	DHB8_STRCM
45	267	20.5	247	1	FABG_MYCTU
46	266.5	20.4	336	1	TS2_MAIZE
47	265.5	20.4	241	1	PHBB_RTIME
48	262	20.1	256	1	BUDC_KLEPN
49	262	20.1	261	1	DHGA_BACME
50	261	20.0	258	1	DHG2_BACSU
51	260	19.9	261	1	DHG3_BACME
52	260	19.9	261	1	DHG2_BACME
53	259	19.9	261	1	YOXD_BACSU
54	258.5	19.8	238	1	DHG1_BACME
55	258	19.8	261	1	DHG1_BACME
56	257	19.7	261	1	FABG_RICPR
57	256.5	19.7	241	1	DHG2_BACSU
58	255	19.6	261	1	FGDH_HUMAN
59	254.5	19.5	256	1	Y4MP_RHISN
60	252	19.3	263	1	ACT3_STRCO
61	251.5	19.3	261	1	SORD_KLEPN
62	251.5	19.3	267	1	3BHD_COMTE
63	250.5	19.2	253	1	YHXC_BACSU
64	249.5	19.1	285	1	NODG_RHIS3
65	247.5	19.0	245	1	GNO_GLOOX
66	247	18.9	256	1	YV06_PSEAE
67	244.5	18.8	262	1	YV06_PSEAE
68	244	18.7	255	1	HDHA_ECOLI
69	243	18.6	255	1	BDHA_ECOLI
70	243	18.5	270	1	BDHA_RHIME
71	241.5	18.5	258	1	FABG_MYCAT
72	241	18.5	255	1	YGCW_ECOLI
73	240.5	18.4	247	1	FABG_PSEAE
74	240	18.4	248	1	FABG_CHLPP
75	240	18.3	257	1	YXUF_BACSU
76	239	17.8	245	1	NODG_RHIME
77	232.5	17.8	273	1	TRNL_DANST
78	229.5	17.6	894	1	FOX2_NEUCR
79	229	17.6	249	1	DHK2_STEVN
80	228.5	17.5	258	1	BDHA_ALCEU
81	228.5	17.5	254	1	IDNO_ECOLI
82	226	17.3	242	1	PHAB_PARDE
83	225.5	17.3	256	1	DH80_RHOSH
84	225.5	17.3	255	1	FABG_MYCSM
85	225	17.3	255	1	MTDH_UROFA
86	224.5	17.2	256	1	SRUD_ECOLI
87	223.5	17.1	259	1	BUDC_KLETE
88	223	17.1	241	1	FOX2_YEAST
89	222.5	17.1	900	1	KDUD_ECOLI
90	221.5	17.0	253	1	DHK1_STEVN
91	221.5	17.0	272	1	KDUD_BACSU
92	221	16.9	254	1	GS39_BACSU
93	220.5	16.9	285	1	Y452_LISIN
94	219	16.8	248	1	FABG_ACTRA
95	215	16.5	242	1	YAY8_SCHPO
96	214.5	16.4	286	1	YAXD_BACSU
97	214	16.4	299	1	YALA_RHISN
98	213.5	16.4	278	1	DHB8_CALVA
99	213	16.3	134	1	Y432_LISMO
100	213	16.3	248	1	P19337_eubacterium

ALIGNMENTS

HCD2_HUMAN STANDARD; PRT; 261 AA.

AC Q99714; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) (Short-chain type dehydrogenase/reductase KH96G2).

GN HADH2 OR ERAB OR KH96G2 OR SCHAD.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

XX [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Brain;

RA MEDLINE=97478528; PubMed=9338779;

RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F., Collins K., Zhu A., Stern E., Saldo T., Tohyama M., Ogawa S., Roher A., Stern D.;

RA "An intracellular protein that binds amyloid-beta peptide and mediates neurotoxicity in Alzheimer's disease.";

RT Nature 389:689-695(1997).

RL [2]

RP SEQUENCE FROM N.A.

RA Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA MEDLINE=98337980; PubMed=9671743;

RA Miller A.P., Willard H.F.;

RT "Chromosomal basis of X chromosome inactivation: Identification of a multigene domain in Xp11.21-p11.22 that escapes X inactivation.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).

RN [4]

RP SEQUENCE FROM N.A.

RA TISSUE-Brain;

RA MEDLINE=98221216; PubMed=9553139;

RA He X.Y., Schulz H., Yang S.Y.;

RT "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical to an amyloid beta-peptide-binding protein involved in Alzheimer's disease.";

RL J. Biol. Chem. 273:10741-10746(1998).

RN [5]

RP SEQUENCE FROM N.A.

RA TISSUE-Lung;

RA Strausberg R.;

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION ASSOCIATED WITH ALZHEIMER DISEASE.

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS OVEREXRESSED IN NEURONS AFFECTED IN AD.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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CC -----

DR EMBL; U96132; AAC51812.1; -

DR EMBL; U73514; AB68858.1; -

DR EMBL; AF069134; AAC39900.1; -

DR EMBL; AF035555; AAC15902.1; -

DR EMBL; AF037438; AAC16419.1; -

DR EMBL; BC000372; AAH00372.1; -

DR HSSP; 070351; 1E3S.

DR Genew; HGNC:4600; HADH2.

DR MIM; 300256; -

DR InterPro; IPR002198; ADH_short.

DR Pfam; PF00106; adh_short; 1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NAD.

FT NP_BIND 12 37 NAD (BY SIMILARITY).

FT ACT_SITE 168 168 BY SIMILARITY.

SO SEQUENCE 261 AA; 26923 MW; 9E74F242E3E6EF1 CRC64;

Query Match 99.6%; Score 1299; DB 1; Length 261;

Best Local Similarity 99.6%; Pred. No. 4,3e-93;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAARSVKGLAVITGASGIGTAFARLVGGASAVLLDLPNSGGEAOKKIGNCVF 60

DB 1 MAAARSVKGLAVITGASGIGTAFARLVGGASAVLLDLPNSGGEAOKKIGNCVF 60

QY 61 APADYTSERDVOTATLAKGKFGKRVAVNCAGIYVASKTYNKKGTHTLEDFORLV 120

DB 61 APADYTSERDVOTATLAKGKFGKRVAVNCAGIYVASKTYNKKGTHTLEDFORLV 120

QY 121 NLMGFNVRILVAGENGONEPDGGQGVITNTASVAAPFGVQGAASAKGIVGWL 180

DB 121 NLMGFNVRILVAGENGONEPDGGQGVITNTASVAAPFGVQGAASAKGIVGWL 180

QY 181 PIARDIAPIGIRVMTIAPLFGTPTLTSPKVSNFLASQVFPFRLDPAEYATLVQAI 240

DB 181 PIARDIAPIGIRVMTIAPLFGTPTLTSPKVSNFLASQVFPFRLDPAEYATLVQAI 240

QY 241 IENPFLNGEYIRLDGAIKRP 261

DB 241 IENPFLNGEYIRLDGAIKRP 261

RESULT 2

HCD2_BOVIN STANDARD; PRT; 261 AA.

AC Q02651; 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).

GN HADH2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-Liver;

RA MEDLINE=97214648; PubMed=9061028;

RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;

RT "Cloning and expression of cDNA for a newly identified isozyme of bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into mitochondria.";

RL Biochim. Biophys. Acta 1350:317-324(1997).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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CC -----

DR EMBL: AB002156; BAA19510.1; -

DR HSPB: 070351; 1B6W.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NAD; Mitochondrion.

FT NP_BIND 12 37 NAD (BY SIMILARITY).

FT ACT_SITE 168 168 BY SIMILARITY.

SQ SEQUENCE 261 AA; 27140 MW; 8C7572B6A9A49780 CRC64;

Query Match 92.6%; Score 1208; DB 1; Length 261;

Best Local Similarity 92.0%; Pred. No. 4.3e-86;

Matches 240; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAAACRSYKGLVAVITGASGLGATATKRLVGGASAVLLDPLNSGGEAOKLGNVCYF 60

DB 1 AAAACRSYKGLVAVITGASGLGATATKRLVGGASAVLLDPLNSGGEAOKLGNVCYF 60

QY APADVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120

DB 61 APADVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120

QY 61 APADVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120

DB 121 NMGTENVIRLVAGEQNEPDGOGGQGVIIINTASVAAFEGVGQAAYSAKSGIVGNTL 180

DB 121 NMGTENVIRLVAGEQNEPDGOGGQGVIIINTASVAAFEGVGQAAYSAKSGIVGNTL 180

DB 121 NMGTENVIRLVAGEQNEPDGOGGQGVIIINTASVAAFEGVGQAAYSAKSGIVGNTL 180

QY 181 PIADLPDPIGRVNTIAPGLFGPPLTSLPEKYSNPLASQVPPSRIGDPAEYAHVQAT 240

DB 181 PIADLPDPIGRVNTIAPGLFGPPLTSLPEKYSNPLASQVPPSRIGDPAEYAHVQAT 240

QY 241 IENPFLNGEVIRLDGAIKMP 261

DB 241 IENPFLNGEVIRLDGAIKMP 261

RESULT 3

HCD2_RAT

ID HCD2_RAT STANDARD; PRT; 260 AA.

AC 070351; Q8QYD4;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR ERAB.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RP TISSUE=Liver;

RA "Rattus norvegicus amyloid beta-peptide binding protein (ERAB) mRNA."

RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RP STRAIN=Sprague-Dawley; TISSUE=Brain;

RA Yang S.-Y., He X.-Y.;

RT "Molecular cloning and characterization of the cDNA of rat brain short chain L-3-hydroxyacyl-CoA dehydrogenase."

RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.

RN [3]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC TISSUE=Brain;

RC MEDLINE=20481418; PubMed=11023795;

RA Powell A.J., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D., Lustbader J., Stern A.R., Stern D.M., Brady R.L.;

RT "Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding alcohol dehydrogenase (ABAD)."

RT J. Mol. Biol. 303:311-327(2000).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.

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CC -----

DR EMBL: AF048878; AAC05747.1; -

DR EMBL: AF069770; AAF14853.1; -

DR PDB: 1E3W; 25-MAY-01.

DR PDB: 1E3S; 25-MAY-01.

DR PDB: 1E6W; 25-MAY-01.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT; 1.

KW Oxidoreductase; NAD; Acetylation; 3D-structure.

FT INIT MET 0 0 BY SIMILARITY.

FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).

FT NP_BIND 11 36 NAD (BY SIMILARITY).

FT ACT_SITE 167 167 BY SIMILARITY.

FT CONFLICT 4 4 V -> C (IN REF. 2)

SQ SEQUENCE 260 AA; 27114 MW; 30E7E73A95F9227 CRC64;

Query Match 88.4%; Score 1153; DB 1; Length 260;

Best Local Similarity 87.7%; Pred. No. 7.3e-82;

Matches 228; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 2 AAAACRSYKGLVAVITGASGLGATATKRLVGGASAVLLDPLNSGGEAOKLGNVCYF 61

DB 1 AAAACRSYKGLVAVITGASGLGATATKRLVGGASAVLLDPLNSGGEAOKLGNVCYF 60

QY 62 PAVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 121

DB 61 PAVTSEKDVQATLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120

QY 122 LMGTENVIRLVAGEQNEPDGOGGQGVIIINTASVAAFEGVGQAAYSAKSGIVGNTL 181

DB 121 LMGTENVIRLVAGEQNEPDGOGGQGVIIINTASVAAFEGVGQAAYSAKSGIVGNTL 180

QY 182 IARDLPDPIGRVNTIAPGLFGPPLTSLPEKYSNPLASQVPPSRIGDPAEYAHVQAT 241

DB 181 IARDLPDPIGRVNTIAPGLFGPPLTSLPEKYSNPLASQVPPSRIGDPAEYAHVQAT 240

QY 242 IENPFLNGEVIRLDGAIKMP 261

DB 241 IENPFLNGEVIRLDGAIKMP 260

RESULT 4

HCD2_MOUSE

ID HCD2_MOUSE STANDARD; PRT; 261 AA.

AC 008756;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR HSD17B10 OR ERAB.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C57BL/6 X CBA;
 CC Fu J., Chen X., Stern D., Yan S.D.;
 CC Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -1 CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1 SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U96116; AAB57689.1; ALT_INIT.
 CC DR HSSP: 070351; 1B6W.
 CC DR SWISS-2DPAGE: 008756; MOUSE.
 CC DR MGD: MGI:133871; Hsd17b10.
 CC DR InterPro: IPR002198; ADH_short.
 CC Pfam: PF00106; adh_short.1.
 CC DR PRINTS: PR00080; SDRFAMILY.
 CC PROSITE: PS00061; ADH_SHORT; 1.
 CC KM Oxidoreductase; NAD.
 CC FT NP_BIND 12 37 NAD (BY SIMILARITY).
 CC ACT_SITE 168 168 BY SIMILARITY.
 CC FT SEQUENCE 261 AA; 27418 MW; 61213B13E2839D41 CRC64;

Query Match 87.0%; Score 1134; DB 1; Length 261;
 Best Local Similarity 86.2%; Pred. No. 2.1e-80;
 Matches 225; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MAACRSYKGLVAVITGASGLGLATRLVGGASAVLDDLPSSGGEAQAQKKNACVE 60
 DB 1 MAAAVRSYKGLVAVITGASGLGLATRLVGGASAVLDDLPSSGGEAQAQKKNACVE 60
 QY 61 APADVTSEKDYQALALAKGFGFRVDVAVNAGAVASKTYNNLKKGQTHLEDRVLVD 120
 DB 61 APADVTSEKDYQALALAKGFGFRVDVAVNAGAVASKTYNNLKKGQTHLEDRVLVD 120
 QY 121 NLMGTFNIRLVAGMGONPEPDGQGORVINTASVAAFEQGVCAAYASAKSGIYAKTL 180
 DB 121 NLMGTFNIRLVAGMGONPEPDGQGORVINTASVAAFEQGVCAAYASAKSGIYAKTL 180
 QY 181 PIARDLPIGIRVMTIAPGLTGTPLTSLPKVSNFTLASQVPEPSRLGDPREAVHVLQAI 240
 DB 181 PIARDLPIGIRVMTIAPGLTGTPLTSLPKVSNFTLASQVPEPSRLGDPREAVHVLQAI 240
 QY 241 IENPLNGEIVIRLDGAIKMP 261
 DB 241 IENPLNGEIVIRLDGAIKMP 261

RESULT 5

HSD2_DROME STANDARD; PRT; 255 AA.
 AC 018404;

DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
 DE (Scully protein).
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 CC [1]
 CC SEQUENCE FROM N.A. AND MUTAGENESIS OF LEU-33 AND PHE-120.
 CC STRAIN=Canton-S;
 CC MEDLINE=98252852; PubMed=9585418;
 CC Torroja L., Ortuno-Sanagu D., Ferrus A., Hemmerle B., Barbas J.A.;
 CC Scully, an essential gene of Drosophila, is homologous to mammalian
 CC mitochondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid-beta
 CC peptide-binding protein.
 CC J. Cell Biol. 141:1009-1018(1998).

CC SEQUENCE FROM N.A.
 CC STRAIN=Beckley;
 CC MEDLINE=20196006; PubMed=10731132;
 CC Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 CC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 CC Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 CC Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
 CC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 CC Anil J.F., Agdave A., An H.-J., Andrews-Frannkoc C., Baldwin D.,
 CC Ballaw R.M., Basu N., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 CC Beeson R.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
 CC Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 CC Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 CC Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 CC de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 CC Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunker B.C., Dunn P.,
 CC Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 CC Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 CC Glodek A., Gong F., Goate J.H., Gu Z., Guan P., Harris M.,
 CC Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 CC Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 CC Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 CC Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 CC Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 CC Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 CC Merkulov G., Malsbina N.V., Modarri C., Morris J., Mostrel A.,
 CC Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L.,
 CC Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacle J.M.,
 CC Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 CC Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 CC Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 CC Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 CC Sytkas R., Teator C., Turner R., Venter E., Wang A.H., Wang X.,
 CC Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 CC Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 CC Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 CC Zheng X.H., Zhong F.N., Zhong G.M., Zhou X., Zhu S., Zhu X., Smith H.O.,
 CC Gibbs R.A., Myers E.W., Rubin G.M., Venter T.C.;
 CC "The genome sequence of Drosophila melanogaster."
 CC Science 287:2185-2195(2000).
 CC -1 FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.
 CC -1 CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1 SUBUNIT: MULTIMER (POTENTIAL).
 CC -1 SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1 TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS. HIGHEST
 CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES
 CC AND TESTES.
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Y15102; CA975377.1; -

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Hatt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher R.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.:
 "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of *Thermotoga maritima*."
 RL Nature 393:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC -----
 CC EMBL; AE001811; A036790.1; -
 DR HSSP; P50162; IAE1.
 DR TIGR; TML724; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis: Oxidoreductase; NADP. Complete proteome.
 KW NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACET_SITE 154 154 BY SIMILARITY.
 FT SEQUENCE 246 AA; 26401 MW; 8C08904D28099142 CRC64;
 SQ
 Query Match 26.3%; Score 343; DB 1; Length 246;
 Best Local Similarity 33.7%; Pred. No. 1,4e-19;
 Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;
 QY 8 VKGLAVITGASGLGATFAERLYVGCGASAVLLDLPNSGGEA---QAKRLGNVCFPAD 64
 DB 3 LEGVCLITGAASIGKATILLFAGEBQATVIAGDISKENDSLYKEBGLPGKVDPLYLN 62
 QY 65 VTSKSDVOTALALAKGFRGVAVANCAGIYAVSKTYNLKGGQTHLEDFQYLVAVNLG 124
 DB 63 VTDDQIKKEVEKVEKVGKGRIDVLYNNAIGTRDALVYRKE-----EDMDAVINVLKG 116
 QY 125 TENYIRLVAGEMGNEPDGQGRVITNTASVAFBEGVOGAASAKSGIYGTLPAR 164
 DB 117 VFNVTQNVVPMIQ-----RNGSIYVSSVGIYINPGQTNVAAKAGVITGMTKWK 170
 QY 185 DLADIGIRVMTIADGLFETPLTSLPEKVSNFLASQVFPFSLDPAEYALV--QALIE 242
 DB 171 ELAQRNIRVNAVAGFETETPMTKLPKARETALSRIPL--GREGKPREVAQVILFLASDE 229
 QY 243 NPELNGEYIRLDGAI 257
 DB 230 SYIVTGVIIGIDGL 244

OC Spermatozoa; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Myrtales; Lythaceae; Cuphea.
 OC NCBI_TaxID=3930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92293104; PubMed=1376402;
 RA Klein B., Pawlowski K., Hoeircke-Grandpierre C., Schell J.,
 RA Toepfer R.:
 RT "Isolation and characterization of a cDNA from *Cuphea lanceolata*
 RT encoding a beta-ketoacyl-ACP reductase."
 RL Mol. Gen. Genet. 233:122-128(1992).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
 CC PLASTIDS.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X64566; CAA5866.1; -
 DR PIR; S19832; S19832.
 DR HSSP; P50162; IAE1.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;
 KW Transit peptide.
 FT TRANSIT 1 61
 FT CHAIN 62 320
 FT NP_BIND 82 106 CHLOROPLAST (BY SIMILARITY).
 FT ACET_SITE 227 227 3-OXOACYL-[ACYL-CARRIER PROTEIN]
 FT SEQUENCE 320 AA; 33103 MW; 06BAF052282B8C87 CRC64;
 SQ
 Query Match 25.9%; Score 338; DB 1; Length 320;
 Best Local Similarity 32.7%; Pred. No. 4,6e-19;
 Matches 87; Conservative 47; Mismatches 110; Indels 22; Gaps 6;
 QY 2 AAACRKYKLVAVITGASGLGATFAERLYVGCGASAVLLDLPNSGGEA---QAKRLGN 56
 DB 69 AGAGQVSESPVAVITGASGLGKALILSL--GAGCKVLYNVARSSKEBEYSKETLEAG 127
 QY 57 NCFEADADYTSKEDVOTALALAKGFRGVAVANCAGIYAVSKTYNLKGGQTHLEDFQ 116
 DB 128 QALTEGVDYSKEDVYAMIKTAVDAMGTVDVLYNNAIGTRDGLLRMKKSSQ-----WQE 181
 QY 117 VLDVNLMTGFNNYIRLVAGEMGNEPDGQGRVITNTASVAFBEGVOGAASAKSGIY 176
 DB 182 VIDLNTGVFLCTQAAAKIMKK-----KKRIINIASVGLVGNAGQANTSAKAGVI 235
 QY 177 GMTLPARDLAPIGIRVMTIADGLFETPLTSLPEKVSNFLASQVFPFSLDPAEYALV 236
 DB 236 GEFKTVARAYASANINIVNAVAPGISSDMTSLGDDINKKILLETIPL--GRYGQPREVAVGL 294
 QY 237 VQAIENP---PLNGEYIRLDGAI 259
 DB 295 VERLAINPASSVYTGQVFTIDGGM 320

RESULT 9
 DHB8_HUMAN
 ID DHB8_HUMAN STANDARD; PRT; 261 AA.

AC Q92506; Q9UIQ1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-
 beta-hydroxysteroid dehydrogenase 8) (K6 protein) (K6-6).
 GN HSD17B8 OR HKE6 OR RING2 OR FABG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tubby B.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 3-261 FROM N.A.
 RX MEDLINE=97001166; PubMed=8812499;
 RA Ando A., Kikuchi Y.Y., Shigenari A., Kawata H., Okamoto N., Shitina T.,
 Chen L., Ikemura T., Abe K., Kimura M., Inoko H.;
 RT "cDNA cloning of the human homologues of the mouse K6 and K6 genes
 at the centromeric end of the human MHC region.";
 RL Genomics 35:600-602(1996).
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone +
 NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS,
 LOWER IN THE SKELETAL MUSCLE AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AL031228; CAC88444.1; -;
 DR EMBL: D82061; BA01529.1; -;
 DR HSSP: 070351; 1E6W.
 DR Genew: HGNC:3554; HSD17B8.
 DR MIM: 601417; -;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.
 KW NP_BIND
 FT ACT_SITE 169 169 NAD (BY SIMILARITY).
 FT CONFLICT 117 117 E -> R (IN REF. 2).
 FT CONFLICT 193 193 R -> P (IN REF. 2).
 FT CONFLICT 208 208 Q -> K (IN REF. 2).
 FT CONFLICT 212 212 Q -> K (IN REF. 2).
 SQ SEQUENCE 261 AA; 26574 MW; 888B2D731714D71 CRC64;
 Query Match 25.4%; Score 331.5; DB 1; Length 261;
 Best Local Similarity 31.2%; Pred. No. 1,1e-18;
 Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
 QY 8 VKGLVAVITGGASGLGATAPRLVGGASAVLLDLPNSGGEAQAQK-----GN 56
 DB 9 LRSALAVTGGASGLGATAPRLVGGASAVLLDLPNSGGEAQAQK-----GN 68
 QY 57 NCVAPADVTSEKVOVALALAKGKGR-DVAVNVCAGIIVASKTYNLKKGQHTLLEDFQ 115
 DB 69 HAAP-QADVSEARARCLLEQVACFSRPSVYVSCAGITQDEFILHSE-----DDWD 121
 QY 116 RVLDVLMGTFNVIRLVAGENGQNEPDGGQGVYITWASVAAFEGVGOAAYSASKG 175
 DB 122 KVIIVNKGITLVTAQAQALVSN-----GGRGIIINISSIVKGVGVGQNTVAASAGV 176

QY 176 VQGLTPIARDLAPIGIRVWTAPGLGPELLSLPEKYNFNLASQVPPSRGLDPAEYAH 235
 DB 177 IGLTQIARELHGRHGRNCSVLPGLFAPDMTQKQVYDKITTEMIPM-GHLGDEYAD 235
 QY 236 LVQ--AIIEPFLNGEVIRLDGAIRM 259
 DB 236 VVAFLASEDSGYITGTSVEVTGLFWM 261
 RESULT 10
 FABG_VIBCH STANDARD; PRT; 244 AA.
 AC Q9KH7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 acyl carrier protein reductase).
 GN FABG OR VC2021.
 OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OC NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EI for N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
 Gill S.R., Nelson K.E., Read J.D., Tettelin H., Richardson D.,
 Esmailova M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellars P.,
 McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RT Nature 406:477-483(2000).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 NAD(P)(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
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 CC -----
 DR EMBL: AE004276; AAF95169.1; ALT_INT.
 DR HSSP: P19992; 1HDC.
 DR TIGR: VC2021; 1HDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PRO0080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT ACT_SITE 151 151 NADP (BY SIMILARITY).
 FT ACT_SITE 151 151 BY SIMILARITY.
 SQ SEQUENCE 244 AA; 25566 MW; 9FB2E827BD7CC3CE CRC64;
 Query Match 25.3%; Score 330.5; DB 1; Length 244;
 Best Local Similarity 32.0%; Pred. No. 1.3e-18;
 Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;
 QY 7 SVKGLVAVITGGASGLGATAPRLVGGASAVLLDLPNSGGEAQAQKGNKCVFAPADVT 66
 DB 2 NLEKVALVITGGASGLGATAPRLVGGASAVLLDLPNSGGEAQAQKGNKGNKCVFAPADVT 61
 QY 67 SEKDVTALALAKGKGRDVAVNVCAGIIVASKTYNLKKGQHTLLEDFQVLDVLMGTF 126

RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Aaevedo V., Bertero M.G., Bessieres P., Bolocin A., Borchert S.,
 RA Borris R., Bourlier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denhart D., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Ertan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallazzi A., Gallero N.,
 RA Gilm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kunnano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Meuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Portwolk S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Solod B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Valari A., Wandt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Watters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis." Nature 390:249-256(1997).
 RL [3]
 RN SEQUENCE OF 1-172 FROM N.A.
 RP MEDLINE=98195738; PubMed=9534248;
 RX Foulger D., Errington J.,
 RA "A 28 kbp segment from the spvcm region of the Bacillus subtilis 168
 RT genome." Microbiology 144:801-805(1998).
 RL [4]
 RN SEQUENCE OF 230-246 FROM N.A.
 RP STRAIN=168;
 RA Oguro A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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CC EMBL: U59433; AAC4307.1; -
 DR EMBL: 299112; CAB13464.1; -
 DR EMBL: Y13937; CAAT4250.1; -
 DR EMBL: D64116; BAA10974.1; -
 DR HSSP: Q12634; IYBY; -
 DR Subtilist; BG1535; fabc;
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 9 33 NADP (BY SIMILARITY).
 FT ACT_SITE 154 154
 FT CONFLICT 23 23 D -> A (IN REF. 1).

SQ SEQUENCE 246 AA; 26282 MW; C6A391167D3237DC CRC64;
 Query Match 24.0%; Score 312.5; DB 1; Length 246;
 Best Local Similarity 29.7%; Pred. No. 3,1e-17;
 Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;
 QY 13 AITGCGASGLGATMERLVGCGASVLLDLPNGGSEAA-----KTLGNVCAPADV 65
 DB 7 AIVTASRSGISILDLAKSASAVV---VNTSGEAAANEVDEIKMGKALVADV 63
 QY 66 TSEKDVOTALALAKGFRGVDAVAVACIAVASKYTNKRGQHTLEDFOYLDVNLGT 125
 DB 64 SNPEVDVNMKRTLSVFSFTIDLVNNAGITRDLNLRMKE-----DEMDDVINLKGV 117
 QY 126 FNVILVAGEMQNPDDGGGQGVITINASVAAPFGQVGOAASAKSGIYGMTPARD 185
 DB 118 FNGTAAVTRQMKQ-----RSGRITVNSIYGVSGNPGQAVYAAKGVIGLKSSAKE 171
 QY 186 LAPIGIRVWTIAPGLFTPLLTSLPEKYSNFLASGVPPSPRLGPAEYAHVQAIIEN-- 243
 DB 172 LASRNTVNAIAPGISTIDMTDKLAKVDDEMLKQIPL-ARGPESDVSVYTFASGA 230
 QY 244 PFLNGEVRFDGAIK 259
 DB 231 RYMTGGTTHIDGMV 246
 RESULT 13
 ID FAGL_SINY3 STANDARD; PRT; 247 AA.
 AC P73574;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase 1 (EC 1.1.1.100) (3-
 DE ketocacyl-acyl carrier protein reductase 1).
 GN FMBGI OR SKR0886.
 OS Synecocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 OX NCBI_Taxid=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiyama S., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Mureki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions." J.
 RL DNA Res. 3:109-136(1996).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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CC EMBL: D90907; BAA17614.1; -
 DR EMBL: P50162; IAE1.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.

KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 11 NADP (BY SIMILARITY).
 ACT_SITE 156 BY SIMILARITY.
 SQ SEQUENCE 247 AA; 25724 MM; 91EEF9409C777E20 CRC64;

Query Match 24.0%; Score 312.5; DB 1; Length 247;
 Best Local Similarity 32.1%; Pred. No. 3.1e-17;
 Matches 85; Conservative 45; Mismatches 92; Indels 43; Gaps 8;

QY 12 VAVITGGASGLGATLAEFLVGQ-----ASVLLDLPNSGGEAOKKLGNNC 58
 DB 8 VALVTGASRGIGATLALANQMKVYVNTAOSSTADYVAEILNGSEA----- 58
 QY 59 VFAPADVTSEKDYQATALAKGKFGVDVAVNCAGIAVASKTYNLEKGGTHLEDFQRYL 118
 DB 59 IAVOAVNANDEVDOLIKTTDKFSRIDVLVNNAGITRDITLLRMK-----LEDMQAVI 112
 QY 119 DVNLMGFENYIRLVAGMGONEPDGOGGVIIINTSVAFEGVQGAAYASAKSGIVGM 178
 DB 113 DNLGTGFLCTKAVSKIMLKQ-----KSGRIINTSVAGMGNPCQANYSAAKAGVITGF 166
 QY 179 TLEPIADLAFIGIRVMTIAPGLFGLPFLSL-PEKYSNFLASQVPPSRIGDPAEYAHLV 237
 DB 167 TKVYAKELASRGTVANVAPGFATDMETENLNEPIIQF-----IPL-ARYGQPEEVAAGTI 221
 QY 238 QALIENP---FLNGEYIRLDGATRM 259
 DB 222 RFLATDPAAAVITGQTFPNDGKVM 246

RESULT 14

YK02_MYCTU STANDARD; PRT; 260 AA.
 AC Q10855;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative oxidoreductase RV2002 (EC 1.1.1.1).
 GN FABG3 OR RV2002 OR MT2058 OR MTCY39.16C.
 OS Mycobacterium tuberculosis.
 CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Baddock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagsals K., Kirogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RL complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolova M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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DR EMBL; 274025; CA98414.1; -
 DR EMBL; AE007057; AAK46335.1; -
 DR HSSP; P19992; IHDC.
 DR TIGR; MT2058; -
 DR TubercuList; RV2002; -
 DR InterPro; IPR002198; ADL_short.
 DR Pfam; PF00106; adl_short; 1.
 DR PRINTS; PR00080; SDRFAMLY.
 DR PROSITE; PS00061; ADL_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT NP_BIND 11 NAD (BY SIMILARITY).
 FT ACT_SITE 153 BY SIMILARITY.
 FT CONFLICT 174 S -> G (IN REF. 2).
 SQ SEQUENCE 260 AA; 27030 MM; 0935A14ED36220B7 CRC64;

Query Match 23.4%; Score 305; DB 1; Length 260;
 Best Local Similarity 33.9%; Pred. No. 1.2e-16;
 Matches 85; Conservative 41; Mismatches 99; Indels 26; Gaps 5;

QY 10 GIVAVITGGASGLGATLAEFLVGQASAVLLDLPNSGGEAOKKLGNNCVFAPADVTSEK 69
 DB 7 GRVALVSGGARGMGSHVRANVABGAKVYFDDIDDESKAAVAELADARVHVDYQPA 66
 QY 70 DVQATALAKGKFGVDVAVNCAGIAVASKTYNLEKGGTHLEDFQRYLVNMGTEVVI 129
 DB 67 QMTAAVDAVTAFTAGFLHVLVNNAGI-----LNTGTDIDVATLQRIIDVNLGVFLGI 120
 QY 130 RLVAGMGONEPDGOGGVIIINTSVAFEGVQGAAYASAKSGIVGMTPIRADAPI 189
 DB 121 RAVV-----KMKRAGRSITINISIEGLMGTAVACHYITKRVRSITSTALEGPS 174
 QY 190 GIVMTIAPGLFGLPFLSL-PEKYSNFLASQVPPSRIG---DPAEYAHLV-QALIENP 244
 DB 175 GIVNYSIHGVLKTFMTDMPEDT-----FQIALGRAAEVPEVSNLVVYASDESS 225
 QY 245 FLNGEYIRLDG 255
 DB 226 YSTGAEFVVDG 236

RESULT 15

YMPD_BACSU STANDARD; PRT; 255 AA.
 ID YMPD_BACSU
 AC P39640;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase ympD (EC 1.1.1.1).
 GN YMPD OR IPA-82D.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020537; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coucard M.P., Gonzales W.,
 RA Hillo M.F., Ionescu M., Lubochinsky B., Marcelino L., Mosser I.,
 RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
 RA Rapoport G., Danchin A.;
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97
 RT kb region from 325 degrees to 333 degrees."
 RL M01. Microbiol. 10:371-384(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;

RA MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azavedo V., Bertero M.G., Bessieres P., Bolotin A., Borbott S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuno V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Erington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallen N.,
RA Ghim S.Y., Glaser P., Goffeau A., Goldlighty E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haeche U., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaber-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nodack M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Portolillo S., Prescott A.M.,
RA Priesen E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takeman K.,
RA Takuchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,
RA Toseo V., Uchlyama S., Vandenbol M., Vannier P., Vassartoli A.,
RA Vitali A., Wandut R., Wedler E., Wedler H., Wetzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*".
RT Nature 390:249-256(1997).
RL Nature 390:249-256(1997).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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CC
CC EMBL: X73124; CA51638.1;
CC EMBL: 299123; CAB15799.1;
CC PIR: S39737; S39737.
CC HSP: P50162; IAE1.
CC Subtilisin; BG10628; ywif.
CC InterPro: IPR002198; ADH_short.
CC Pfam: PF00106; adh_short.1.
CC PRINTS: PR00080; SDRFAMILY.
CC PROSITE: PS00061; ADH_SHORT.1.
KM Hypothetical protein: Oxidoreductase: Complete proteome.
FT NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 255 AA; 27324 MW; 20AA2255B8B6C9B CRC64;

Query Match 23.3%; Score 304; DB 1; Length 255;
Best Local Similarity 31.7%; Pred. No. 1.5e-16;
Matches 86; Conservative 41; Mismatches 94; Indels 50; Gaps 7;

QY 14 VITGASGIGLATATRLVGGASAVLLDLPNSGGAQAKKLGNNCV-FAPADVTSEKYO 72
D 11 ITTGASGIGYAAVAFGQQAANVVADIIDEAGQAMRKENDRLHFVQDITIDEAQC 70
QY 73 TALALAKGFGVADVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLGTEVIR- 130
D 71 HAVESAVHFGGLDVLINNAIGETIYAPIHEM-----LSDMNKVLQVNLGMLMSHA 124
QY 131 ----LVAGEMQNEPDQGGGVITNTASVAAFEQVGOQAASASKGIVGMLPIADLA 186
D 125 LKHMALAG-----KGNITNTCSVGVIVAMPDIPAYNASKGVGLQITKSMADV 172

QY 187 APIGIRWMTIAPLFGTPL-----LTSLEPKVSNFLASQVPPSRIGDPA 231
D 173 AKQIIVNCVCPQIITIDPLNEKSFLENNEGTLEIKKAKYNPL-----RKGRE 224
QY 232 EYAHVQAITE--NPLNGEVIRFLOCAIRMQ 260
D 225 EIANVWFLASDLSSYMTGSAITADGGYTAQ 255
RESULT 16
2BHD_STREX STANDARD; PRT; 255 AA.
ID 2BHD_STREX
AC P19992;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
OS Streptomyces exfoliatus (Streptomyces hydropneumans).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=1905;
RN [1]
RP SEQUENCE.
RX MEDLINE=90306363; PubMed=2194840;
RA Marekov L., Krook M., Joernvall H.;
RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type.";
RL FEBS Lett. 266:51-54(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=92052211; PubMed=1946424;
RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
RT Rimsay R.L., Orr J.C.;
RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
RT dehydrogenase: a member of a short-chain dehydrogenase family.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
CC -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) = 17-
CC beta-hydroxyandrostane-3-one + NADH.
CC
CC -1- SUBUNIT: HOMOTETRAMER.
CC
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC
CC PIR: S10707; S10707.
CC PDB: 2HSD; 31-AUG-94.
CC PDB: 1HDC; 07-FEB-95.
CC InterPro: IPR002198; ADH_short.
CC Pfam: PF00106; adh_short.1.
CC PRINTS: PR00080; SDRFAMILY.
CC PROSITE: PS00061; ADH_SHORT.1.
KM Oxidoreductase; NAD; Steroid metabolism; 3D-structure.
FT NP_BIND 10 34 NAD (BY SIMILARITY).
FT ACT_SITE 152 152
SQ SEQUENCE 255 AA; 26484 MW; 9CB93CB66AA628D5 CRC64;

Query Match 23.2%; Score 302; DB 1; Length 255;
Best Local Similarity 33.6%; Pred. No. 2.1e-16;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;

QY 8 VKGIVAVITGASGIGLATATRLVGGASAVLLDLPNSGGAQAKKLGNNCVFAPADVTS 67
D 4 LSGTIVITGASGIGLATATRLVGGASAVLLDLPNSGGAQAKKLGNNCVFAPADVTS 63
QY 68 EKDVTALALAKGFGVADVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLGTEVIR- 127
D 64 EEDQRYVAAFAAREFGVADVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLGTEVIR- 117
QY 128 VIRLVAGEMQNEPDQGGGVITNTASVAAFEQVGOQAASASKGIVGMLPIADLA 187
D 118 GMRIVIRAM-----KDAG--GSIVNISAAGLGLALTSTSYGSKMGVRLSKLAAYELG 171
QY 188 PIGIRWMTIAPLFGTPL--TSLEPKVSNFLASQVPPSRIG--DPAEYAHVQAITE-- 242
D 172 TDRIRVNSVHPGKMTYTPMETGTIRGEGNY--PNTPM--GVGNENPDELGAAYVLLSDT 228

QY 243 NPFLNGEVIRLDG 255
Db 229 SSVYTGAEALVDG 241

RESULT 17
YAVI_RHISN STANDARD; PRT; 548 AA.
ID YAVI_RHISN
AC Q53217;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Putative short-chain type dehydrogenase/reductase YAVI (EC 1.-.-.-).
GN YAVI.
OS Rhizobium sp. (strain NGR34).
OC Plasmid sym PNGR234a.
CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OX Rhizobiaceae; Rhizobium.
RN NCBI_TaxID=394;
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RT "Molecular basis of symbiosis between Rhizobium and legumes."; a
RL Nature 387:394-401(1997).
RN SEQUENCE FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR34 using dye terminators and a thermostable 'sequenase': a
RL Genome Res. 6:590-600(1996).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY. CONTAINS TWO DOMAINS.
CC
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CC
CC EMBL; Z68203; CAA92424.1; ALT_INT.
DR EMBL; AE000101; AAB91897.1; -.
DR HSSP; P50163; 2AEI.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 2.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
KW Multifunctional enzyme.
FT DOMAIN 1 250
FT DOMAIN 271 548
FT NP_BIND 12 37 SHORT-CHAIN DEHYDROGENASE/REDUCTASE 1.
FT ACT_SITE 154 154 NAD OR NADP (BY SIMILARITY).
FT NP_BIND 280 304 BY SIMILARITY.
FT ACT_SITE 420 420 NAD OR NADP (BY SIMILARITY).
SQ SEQUENCE 548 AA; 57593 MW; 399598C5DF17C23F CRC64;

Query Match 22.7%; Score 296.5; DB 1; Length 548;
Best Local Similarity 33.6%; Pred. No. 1.3e-15;
Matches 86; Conservative 40; Mismatches 101; Indels 29; Gaps 8;

QY 10 GIVAYITGASGLGATLAEKLVGQASAVLDDLPNSGGEQAOKKGNVCVAPADYSEK 69
Db 9 GIVAYITGAAAGIGALVDIFPAANGDVVAVDLPDSVGIETLGGNLPHEHLGLEVDVSRD 68
QY 70 DVQATLALAKGKFGFQVDAVNCAGI-----AVASKTYNKKGGQTHLEDFORVLDVNLKGT 125
Db 69 DVVALRALLERKFSNIEVLVNNAGIGPTMAATAD-----ALDFORALAINLVGA 119

QY 126 ENVIVLVAGENGQNEPDGQGGQGVITNTASVAAPFEGVQGAAYSAKSGIVGMLPIARD 185
Db 120 YSVACETAKLM-----KPG-----AIVNVAASLAGLGNPKRGAAYSAKSLSTKSLACR 171
QY 186 LAPIGRTVMTIAPLFGTPIILTSLEPKVSNF-----LASQVFPSPRLDPAEYAHLYQ--A 239
Db 172 WASRGIRTYAVAPGVRHPRMVAEL-ERAGKLDVSAIRRRVPL-GRIARPDEIARAVRELA 229
QY 240 IIEPFLNGEVIRLDG 255
Db 230 SAQASYITGSTLVVDG 245

RESULT 18
FABG_VIBHA STANDARD; PRT; 244 AA.
ID FABG_VIBHA
AC P55336;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG.
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN SEQUENCE FROM N.A.
RX MEDLINE=96134997; PubMed=8550484;
RA Shen Z., Byers D.M.;
RT "Isolation of Vibrio harveyi acyl carrier protein and the fabG, acpP,
RT and fabF genes involved in fatty acid biosynthesis."; a
RL J. Bacteriol. 178:571-573(1996).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; U39441; AAC43589.1; -.
DR HSSP: P19992; 1HDC.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP.
FT NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 151 151 BY SIMILARITY.
SQ SEQUENCE 244 AA; 25519 MW; FC41A1G5B8CDMAA CRC64;

Query Match 22.5%; Score 293.5; DB 1; Length 244;
Best Local Similarity 29.8%; Pred. No. 8.9e-16;
Matches 76; Conservative 51; Mismatches 113; Indels 15; Gaps 4;

QY 7 SVKGLAVITGASGLGATLAEKLVGQASAVLDDLPNSGGEQAOKKGNVCVAPADYSEK 66
Db 2 NIEKTLAVTGASRGITRAIAELLVERGAIVITTAISEGAAALISYLGNGGLALNLT 61
QY 67 SEKDVQATALAKGKFGFQVDAVNCAGIAYASTYLNKKGGQTHLEDFORVLDVNLKGT 126
Db 62 DVESEIETLKTINDECAIDILVNNAGITRDNLKMKD-----DEMNDIINTNLPTIY 115
QY 127 NVIRLVAGENGQNEPDGQGGQGVITNTASVAAPFEGVQGAAYSAKSGIVGMLPIARD 186


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Db      116 RSKAVLRGMMK-----RAGRINVSVVGTMNAGQNTNAAAGVIGFTKSNAREV 169
Qy      187 APGIRVMTIAPGFGTPLTSLPEKVSNFLASQVFPSPRLGDPFAEYAHLY--QATLENP 244
Db      170 ASRGVYNTVAPGFIETDMTKALNDQRAATLSNPV-AGRLGDPREIASVAVYLASPEAA 228
Qy      245 FLNGEVIRLDGAI 259
Db      229 YITGETLHVNGMT 243

RESULT 19
FABG_AQUAE STANDARD; PRT; 248 AA.
ID      067610;
AC      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DI      16-OCT-2001 (Rel. 40, Last annotation update)
DE      3-oxoacyl-[acyl-carrier protein] reductase (Ec 1.1.1.100) (3-ketoacyl-
GN      acyl carrier protein reductase).
OS      Aquifex aeolicus.
OC      Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OX      Aquifex.
RN      NCBI_TaxID=63363;
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98196666; PubMed=9537320;
RA      Deckert G., Warren P.V., Gaasterland T., Young W.G., Jenox A.L.,
RA      Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
RA      Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT      "The complete genome of the hyperthermophilic bacterium Aquifex
RT      aeolicus".
RL      Nature 392:353-358(1998).
CC      -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC      NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC      -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC      PATHWAY.
CC      -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC      (SDR) FAMILY.
CC      -----
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CC      -----
CC      EMBL; AE000752; AAC07575.1; .
CC      DR      HSSB; p50163; 2AE1.
CC      DR      InterPro; IPR002198; ADH_short.
CC      DR      Pfam; PF00106; adh_short; 1.
CC      DR      PRINTS; PR00080; SDRFAMILY.
CC      DR      PROSITE; PS00061; ADH_SHORT; 1.
CC      KM      Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
CC      FT      ACET_SITE 157 157 NADP (BY SIMILARITY).
CC      FT      NP_BIND 12 36 NADP (BY SIMILARITY).
CC      SQ      SEQUENCE 248 AA; 26867 MW; 5CFD9EB9AD83F2C5 CRC64;

Query Match 22.5%; Score 293.5; DB 1; Length 248;
Best Local Similarity 30.0%; Pred. No. 9e-16;
Matches 77; Conservative 50; Mismatches 109; Incls 21; Gaps 6;
Qy      8 VGLVAVITGASGLTAERLVGASAVLLDIPNSGGEQAQKLCN---NCVAPA 63
Db      5 LOGKYSLVGSTRIGRAIAERLASAGSVIITGSGERAKVAEEINKKGVKAHYEM 64
Qy      64 DVTSEKDVOTALALAKGKFGKRVDAVNCAGIVASKTYNLKKGQHTLEDFQRYDVNIM 123
Db      65 NLISESINKAFEEIYLVVDGIDILVNNAGITRDLEFLM-----SLIDWEVYLVNLT 118

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Qy      124 GTFNVIIRLVAGEMGQNEPDQGR--GVITNPASVAAPFEGQQAASKSGIVGMTLPI 182
Db      119 GTFELVQNSLRKIR-----QRMGRVNISSVVGFTGNQGVSTTKAGLIEFTSL 171
Qy      183 ARDLAPIGIRVMTIAPGFGTPLTSLPEKVSNFLASQVFPSPRLGDPFAEYAHLYQATIE 242
Db      172 AKELAPRNVLVNNAVAPGFIETDMTKAVLSSEINQXKEQPLP-GRFGSEEVAVNYVLFCS 230
Qy      243 N--PFLNGEVIRLDGAI 257
Db      231 ELASVITGEVHVNGM 247

RESULT 20
FABG_ECOLI STANDARD; PRT; 244 AA.
ID      P25716; P78821;
AC      01-NOV-1992 (Rel. 22, Created)
DT      01-NOV-1992 (Rel. 35, Last sequence update)
DI      16-OCT-2001 (Rel. 40, Last annotation update)
DE      3-oxoacyl-[acyl-carrier protein] reductase (Ec 1.1.1.100) (3-ketoacyl-
GN      acyl carrier protein reductase).
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Escherichia.
RN      NCBI_TaxID=562;
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92210530; PubMed=1556094;
RA      Rawlings M., Cronan J.E. Jr.;
RT      "The gene encoding Escherichia coli acyl carrier protein lies within
RT      a cluster of fatty acid biosynthetic genes".
RL      J Biol. Chem. 267:5751-5754(1992).
CC      [2]
CC      SEQUENCE FROM N.A.
CC      RX      STRAIN=K12 / MG1655;
CC      RX      MEDLINE=97426517; PubMed=9278503;
CC      RA      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
CC      RA      Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
CC      RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
CC      RA      Mau B., Shao Y.;
CC      RT      "The complete genome sequence of Escherichia coli K-12".
CC      Science 277:1234-1238(1997).
CC      [3]
CC      SEQUENCE FROM N.A.
CC      RX      STRAIN=K12;
CC      RX      MEDLINE=97061202; PubMed=8905232;
CC      RA      Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
CC      RA      Iiyama M., Inada T., Itoh T., Kajihara M., Kanehisa K.,
CC      RA      Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
CC      RA      Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
CC      RA      Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
CC      RA      Yano M., Horiiuchi T.;
CC      RT      "A 718-kb DNA sequence of the Escherichia coli K-12 genome
CC      RT      corresponding to the 12.7-28.0 min region on the linkage map".
CC      DNA Res. 3:137-155(1996).
CC      -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC      NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC      -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC      PATHWAY.
CC      -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC      (SDR) FAMILY.
CC      -----
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DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Oxidoreductase ucpa (EC 1.1.1.177).
 DE UCPA OR STM2445 OR STM2682.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_Taxid=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21534948; PubMed=11677609; SGC1412 / ATCC 700720;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.M., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2".
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE OF 204-263 FROM N.A.
 RC SPECIES=S.typhimurium;
 RX MEDLINE=91358382; PubMed=1909324;
 RA Hryniewicz M.M., Kredich N.M.;
 RT "The cysP promoter of *Salmonella typhimurium*: characterization of two
 RT binding sites for CysB protein, studies of in vivo transcription
 RT initiation, and demonstration of the anti-inducer effects of
 RT thiosulfate".
 RL J. Bacteriol. 173:5876-5886(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Kettlewell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT *enterica* serovar Typhi CT18".
 RL Nature 413:848-852(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE008810; AAL21339.1; -;
 DR EMBL: AL627274; CAD07676.1; -;
 DR PIR: A38121; A38121.
 DR styGene: SG10424; ucpa.
 DR InterPro: IPR002198; ADH_short.
 DR Prosite: PS00061; ADH_SHORT; FALSE_NEG.
 DR Oxidoreductase; Complete proteome.
 KW OXIDOREDUCTASE; Complete proteome.
 FT CONFLICT 218 L->M (IN REF. 2).
 FT CONFLICT 258 S->T (IN REF. 2).
 FT CONFLICT 263 V->I (IN REF. 2).
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 DB 61 ADVRFASVQAANAARAKETEGRIDLVNNAACVCRGNFLDMSE-----EDRDFHIDINI 114
 QY 123 MGTENVIRLVAGEQNEPDGOGQGVYIINTASVA--FEGVGAAYASAKSGIYGMPLP 181
 DB 115 KGVNVTFAVLEPEMKRSD-----GRIVMSSVYGDVADPGETAYLSKAATVGLTKS 168
 QY 182 IARDLAPIGIRVMTIAPGLGFTPLTSL-----PEKVSFTLASQVFPFSPRLQDPAEY 233
 DB 169 LAVEYAGSGIRVNAICPGVRRPMAESIARQSNPDPESTYLEMAKAIPL-RLADPLEV 227
 QY 234 AHLVQ--AIENPFINGEYIRLDG 255
 DB 228 GELAAFLASDESSYLTGTQNVIDG 251
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 AC P14697;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetoacetyl-CoA reductase (EC 1.1.1.36).
 GN PHBB.
 OS Alkaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_Taxid=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H16 / DSM 428 / ATCC 17699;
 RX MEDLINE=89359356; PubMed=2670935;
 RA Peoples O.P., Sinskey A.J.;
 RT "Poly-beta-hydroxybutyrate biosynthesis in Alkaligenes eutrophus H16.
 RT Characterization of the genes encoding beta-ketothiolase and
 RT acetoacetyl-CoA reductase".
 RL J. Biol. Chem. 264:15293-15297(1989).
 CC -1- CATALYTIC ACTIVITY: (R)-3-hydroxyacyl-CoA + NADP(+) -> 3-oxoacyl-CoA + NADPH.
 CC -1- PATHWAY: Poly-beta-hydroxybutyrate biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC -----
 CC EMBL: J04987; AAA21973.1; -;
 DR PIR: B34340; RDAALAE.
 DR HSSP: O70351; 1B3S.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR Prosite: PS00061; ADH_SHORT; 1.
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 FT NP_BIND 8 NADP (BY SIMILARITY).
 FT AC_SITE 153 BY SIMILARITY.
 SQ SEQUENCE 246 AA; 26370 MW; AD6739E0F5C93C06 CRC64;

Query Match 22.0%; Score 287; DB 1; Length 263;
 Best Local Similarity 32.2%; Pred. No. 3, 1e-15;
 Matches 85; Conservative 38; Mismatches 105; Indels 36; Gaps 8;

Thu Jun 26 06:55:06 2003

us-09-931-186-23.rapb

Page 1

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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.3333 Seconds
(without alignments)
1388.950 Million cell updates/sec

Title: US-09-931-186-23

Perfect score: 1304

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Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

Published Applications:AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1299	99.6	261	10	US-09-931-186-2 Sequence 2, Appl
4	1299	99.6	261	10	US-09-931-186-8 Sequence 8, Appl
5	1289	98.8	261	10	US-09-931-186-4 Sequence 4, Appl
6	1289	98.8	261	10	US-09-931-186-6 Sequence 6, Appl
7	1136	87.1	227	9	US-09-984-245-245 Sequence 245, App
8	1136	87.1	227	9	US-09-966-262-245 Sequence 245, App
9	1136	87.1	227	9	US-09-983-966-245 Sequence 245, App
10	1136	87.1	227	9	US-10-143-090-245 Sequence 245, App
11	667.5	51.2	388	9	US-09-920-923-41 Sequence 41, Appl
12	331.5	25.4	259	10	US-09-931-186-17 Sequence 17, Appl
13	329.5	25.3	243	10	US-09-815-242-13360 Sequence 1360, A
14	329.5	25.3	243	10	US-09-815-242-13581 Sequence 13581, A
15	321.5	24.7	245	10	US-09-815-242-10921 Sequence 10921, A
16	314	24.1	237	9	US-10-175-696-14 Sequence 14, Appl
17	314	24.1	237	10	US-09-823-901-2 Sequence 2, Appl
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19	302	23.7	247	8	US-09-478-040-8 Sequence 8, Appl
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21	293.5	22.5	262	9	US-10-307-385-6 Sequence 6, Appl
22	293.5	22.5	262	10	US-09-802-853-6 Sequence 6, Appl
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52	286.5	22.0	246	9	US-09-964-847-6 Sequence 6, Appl
53	286.5	22.0	641	9	US-09-964-847-10 Sequence 10, Appl
54	286.5	22.0	641	9	US-09-964-847-19 Sequence 19, Appl
55	286.5	22.0	642	9	US-09-964-847-59 Sequence 59, Appl
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61	275	21.1	251	10	US-09-815-242-10241 Sequence 10241, A
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71	269	20.6	256	10	US-09-954-314-14 Sequence 14, Appl
72	268	20.6	251	9	US-10-272-419-20 Sequence 20, Appl
73	267	20.5	276	9	US-09-944-160-24 Sequence 24, Appl
74	265.5	20.4	252	9	US-09-910-033A-2 Sequence 2, Appl
75	264.5	20.3	258	9	US-10-156-055A-1 Sequence 1, Appl
76	260	19.9	253	10	US-09-815-242-11842 Sequence 11842, A
77	258	19.8	261	10	US-09-971-536-74 Sequence 74, Appl
78	255	19.6	261	10	US-09-940-037A-29 Sequence 29, Appl
79	254.5	19.5	266	9	US-09-981-353-40 Sequence 40, Appl
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93 235 18.0 311 9 US-09-738-626-3819 Sequence 3819, Ap
94 231 17.7 261 10 US-09-815-242-5813 Sequence 5813, Ap
95 228.5 17.5 247 10 US-09-815-242-11342 Sequence 11342, A
96 226 17.3 254 10 US-09-741-669-411 Sequence 411, App
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98 222.5 17.1 900 9 US-10-060-230-15 Sequence 15, Appl
99 222.5 17.1 900 9 US-10-060-230-17 Sequence 17, Appl
100 221.5 17.0 253 10 US-09-815-242-10279 Sequence 10279, A

ALIGNMENTS

RESULT 1
US-09-931-186-23
Sequence 23, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214S
US-09-931-186-23

Query Match 100.0%; Score 1304; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 5.3e-110;
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Sequence 20, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214A
US-09-931-186-20

Query Match 99.8%; Score 1301; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 9.9e-110;
Matches 260; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAACRSYKGLVAVITGGASGLGATAEKLYGQASAVLLDLPNSGGEAOKKIGNCVF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAEKLYGQASAVLLDLPNSGGEAOKKIGNCVF 60
QY 61 APADVTSEKDVQOTALALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFQRYLDV 120
DB 61 APADVTSEKDVQOTALALAKGKFRGVDAVAVNCAGIAVASKTYNLKKGQTHLEDFQRYLDV 120
QY 121 NMGTFFNIRLVAGEMGNEDPQGGQGVIIINTASVAAPFEGQGAASASKGGIVGNTL 180
DB 121 NMGTFFNIRLVAGEMGNEDPQGGQGVIIINTASVAAPFEGQGAASASKGGIVGNTL 180
QY 181 PIARDAPIGIRVMTIAPGLTGLTLLSLPEKYSNFTLASQVFPFSRLGDPREYAHLYOAI 240
DB 181 PIARDAPIGIRVMTIAPGLTGLTLLSLPEKYSNFTLASQVFPFSRLGDPREYAHLYOAI 240
QY 241 IENPFLNGEVIRLDGAIRMOP 261
DB 241 IENPFLNGEVIRLDGAIRMOP 261

RESULT 3
US-09-931-186-2
Sequence 2, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA

APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931.186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2

Query Match 99.6%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 1.5e-109;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEQAOKKLGNNCF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEQAOKKLGNNCF 60
QY 61 APADVTSEKDVQATALAKGKRGVDAVAVNCAGIAVASKTYNKKGGTHLEDFQRYLDV 120
DB 61 APADVTSEKDVQATALAKGKRGVDAVAVNCAGIAVASKTYNKKGGTHLEDFQRYLDV 120
QY 121 NLMGTFNVRILVAGMGONPPDGGGQGVIIINTASVAFAEGVGAAYASASKGIVGNTL 180
DB 121 NLMGTFNVRILVAGMGONPPDGGGQGVIIINTASVAFAEGVGAAYASASKGIVGNTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFGTPLLTSLEPKVSNFLASQVPPSRGDPPEYAHLYOAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFGTPLLTSLEPKVSNFLASQVPPSRGDPPEYAHLYOAI 240
QY 241 IENPFLNGEYIRLDGAIIRMP 261
DB 241 IENPFLNGEYIRLDGAIIRMP 261

RESULT 4
US-09-931-186-8
Sequence 8, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELVIN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: RETTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931.186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 8
LENGTH: 261
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: wild type ERAB
US-09-931-186-8

Query Match 99.6%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 1.5e-109;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEQAOKKLGNNCF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEQAOKKLGNNCF 60
QY 61 APADVTSEKDVQATALAKGKRGVDAVAVNCAGIAVASKTYNKKGGTHLEDFQRYLDV 120
DB 61 APADVTSEKDVQATALAKGKRGVDAVAVNCAGIAVASKTYNKKGGTHLEDFQRYLDV 120
QY 121 NLMGTFNVRILVAGMGONPPDGGGQGVIIINTASVAFAEGVGAAYASASKGIVGNTL 180
DB 121 NLMGTFNVRILVAGMGONPPDGGGQGVIIINTASVAFAEGVGAAYASASKGIVGNTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFGTPLLTSLEPKVSNFLASQVPPSRGDPPEYAHLYOAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFGTPLLTSLEPKVSNFLASQVPPSRGDPPEYAHLYOAI 240
QY 241 IENPFLNGEYIRLDGAIIRMP 261
DB 241 IENPFLNGEYIRLDGAIIRMP 261

RESULT 5
US-09-931-186-4
Sequence 4, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELVIN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: RETTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931.186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 4
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C5V
US-09-931-186-4

Query Match 99.8%; Score 1289; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 1.2e-108;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEQAOKKLGNNCF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAEERLVGGASAVLLDLPNSGGEQAOKKLGNNCF 60
QY 61 APADVTSEKDVQATALAKGKRGVDAVAVNCAGIAVASKTYNKKGGTHLEDFQRYLDV 120
DB 61 APADVTSEKDVQATALAKGKRGVDAVAVNCAGIAVASKTYNKKGGTHLEDFQRYLDV 120

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RESULT 6
US-09-931-186-6
; Sequence 6, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREGO, MELWYN A.
; APPLICANT: AGRETE, CHARLES S.
; APPLICANT: AUSTI, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPICZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; TITLE OF INVENTION: OF INHIBITORS THEREOF
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C58V
US-09-931-186-6

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RESULT 7
US-09-984-245-245
Sequence 245, Application US/09984245
Patent No. US20020165374A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/984,245
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,350
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/050,937
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-245-245

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us-09-931-186-23.rapb

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Best Local Similarity 99.6%; Pred. No. 6,5e-95;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAVLIDLPNSGGEAQAQKKGNNCVPAPADVTSEKDVOTATLAKKFGFVAVNCAGI 94
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Db 1 ASAVLIDLPNSGGEAQAQKKGNNCVPAPADVTSEKDVOTATLAKKFGFVAVNCAGI 60
QY 95 AVASTYLNKKGGQHTLEDFOFVLDVNLMTGFENVIRLVAGEMQNEPDGGQGRVYIINTA 154
    |||||
Db 61 AVASTYLNKKGGQHTLEDFOFVLDVNLMTGFENVIRLVAGEMQNEPDGGQGRVYIINTA 120
QY 155 SVAAFEGVGOAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLFGPTLTSLEPKVS 214
    |||||
Db 121 SVAAFEGVGOAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLFGPTLTSLEPKVC 180
QY 215 NFLASQVPPPSRLGDPAPAYAHVQALITENPFLNGEVIIRLDGAIRMOP 261
    |||||
Db 181 NFLASQVPPPSRLGDPAPAYAHVQALITENPFLNGEVIIRLDGAIRMOP 227

RESULT 8
US-09-966-262-245
; Sequence 245, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
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PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-245

Query Match 87.1%; Score 1136; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 6,5e-95;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAVLIDLPNSGGEAQAQKKGNNCVPAPADVTSEKDVOTATLAKKFGFVAVNCAGI 94
    |||||
Db 1 ASAVLIDLPNSGGEAQAQKKGNNCVPAPADVTSEKDVOTATLAKKFGFVAVNCAGI 60
QY 95 AVASTYLNKKGGQHTLEDFOFVLDVNLMTGFENVIRLVAGEMQNEPDGGQGRVYIINTA 154
    |||||
Db 61 AVASTYLNKKGGQHTLEDFOFVLDVNLMTGFENVIRLVAGEMQNEPDGGQGRVYIINTA 120
QY 155 SVAAFEGVGOAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLFGPTLTSLEPKVS 214
    |||||
Db 121 SVAAFEGVGOAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLFGPTLTSLEPKVC 180
QY 215 NFLASQVPPPSRLGDPAPAYAHVQALITENPFLNGEVIIRLDGAIRMOP 261
    |||||
Db 181 NFLASQVPPPSRLGDPAPAYAHVQALITENPFLNGEVIIRLDGAIRMOP 227

RESULT 9
US-09-983-966-245
; Sequence 245, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-983-966-245
Query Match      87.1%; Score 1136; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 6.5e-95;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      35 ASAYVLDLPNSGGGAQAKKLNCCVFAPADYTSKDVQYALALAKGFGRYDVAVNCAGI 94
      1 ASAYVLDLPNSGGGAQAKKLNCCVFAPADYTSKDVQYALALAKGFGRYDVAVNCAGI 60
DB      95 AVASKTYNLKKGQHTLEDFQRYLDVNLMTGFNVIRLVAGMGONEDPOGGQRYIINTA 154
      61 AVASKTYNLKKGQHTLEDFQRYLDVNLMTGFNVIRLVAGMGONEDPOGGQRYIINTA 120
QY      155 SVAAFEQGYGAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLTSLPERKYS 214
      121 SVAAFEQGYGAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLTSLPERKYS 180
DB      215 NFLASQVPPPSRLGDPAEYAHLYQAIIENPFLNGEVIRLDGAIKRMOP 261
      181 NFLASQVPPPSRLGDPAEYAHLYQAIIENPFLNGEVIRLDGAIKRMOP 227
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RESULT 10
US-10-143-090-245
; Sequence 245, Application US/10143090
; Publication No. US20030069406a1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004Pl
; CURRENT APPLICATION NUMBER: US/10/143,090
; PRIOR APPLICATION NUMBER: 2002-05-13
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRF
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; ORGANISM: Homo sapiens
; US-10-143-090-245
Query Match      87.1%; Score 1136; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 6.5e-95;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      35 ASAYVLDLPNSGGGAQAKKLNCCVFAPADYTSKDVQYALALAKGFGRYDVAVNCAGI 94
      1 ASAYVLDLPNSGGGAQAKKLNCCVFAPADYTSKDVQYALALAKGFGRYDVAVNCAGI 60
DB      95 AVASKTYNLKKGQHTLEDFQRYLDVNLMTGFNVIRLVAGMGONEDPOGGQRYIINTA 154
      61 AVASKTYNLKKGQHTLEDFQRYLDVNLMTGFNVIRLVAGMGONEDPOGGQRYIINTA 120
QY      155 SVAAFEQGYGAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLTSLPERKYS 214
      121 SVAAFEQGYGAAYASASKSGIVGNTLPARDLAPIGIRVMTIAPGLTSLPERKYS 180
DB      215 NFLASQVPPPSRLGDPAEYAHLYQAIIENPFLNGEVIRLDGAIKRMOP 261
      181 NFLASQVPPPSRLGDPAEYAHLYQAIIENPFLNGEVIRLDGAIKRMOP 227
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RESULT 11
US-09-920-923-41
; Sequence 41, Application US/09920923
; Publication No. US20030022273A1
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/09/920,923
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 41
; LENGTH: 388
; TYPE: PRF
; ORGANISM: Flavobacterium sp. R1534
; US-09-920-923-41
Query Match      51.2%; Score 667.5; DB 9; Length 388;
Best Local Similarity 55.5%; Pred. No. 2.6e-52;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;
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Page 7

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Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAR, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOMALTER, RICHARD E.
APPLICANT: TEMPCEYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLARANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931.186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-186-17

Query Match      25.4%; Score 331.5; DB 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 3.2e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;

QY 8 VKGLAVITGASGLIATARIYVGGASAVLIDLPNSGGAQAKL-----GN 56
DB 7 LRSALAVITGASGLIATARIYVGGASAVLIDLPNSGGAQAKL-----GN 56
QY 57 NCVAPADYSEKVOYALALAKGFEGR-VDAVAVNCAIAVASKTYNLKKGQHTLEDFO 115
DB 67 HAAE-QADVSEARARACILEQVQACFSRPSVYVSCAGITQDEFLLHME-----DWD 119
QY 116 RVLVNMGTENVIRIVAGEMGOEPDGGGQGVITNTASVAFEGOVGOAAYSASRGI 175
DB 120 KVIAYNLKGTFLVQAAQALVSN-----GCRSITINSSVGVGVANGVGTNTASAGV 174
QY 176 VGMTLPIARDIAPIGIRVMTIAPGLFGTPLTSLPEKVSNFLASQVPEPSRLDPAEYAH 235
DB 175 IGLTQFARLEGIRGIRONSVLPGFIATPMQKVPQKVDKITEMIM-GHLGDPEDVAD 233
QY 236 LVQ--AILENPELNGEVRIDGAIIRM 259
DB 234 VVAFLASEDSGYITGTSYEVVGLFM 259

RESULT 13
US-09-815-242-13360
Sequence 13360, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815.242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206.848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207.727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242.578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253.625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257.931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269.308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13360
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360

Query Match      25.3%; Score 329.5; DB 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 4.5e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLIATARIYVGGASAVLIDLPNSGGE-----AQAKIGNCVAPADYSE 68
DB 10 ITGASGLIATARIYVGGASAVLIDLPNSGGE-----AQAKIGNCVAPADYSE 68
QY 69 KDVQTLALAKGFGYDVAVNCAIAVASKTYNLKKGQHTLEDFOQRLVDYNTLMTENV 128
DB 66 ADKKRMDIAIALGSDVAVLVNNAAGI--TQDTLMKLM---TEADEKYLKYNLGAFFNM 119
QY 129 IRIVAGEMGOEPDGGGQGVITNTASVAFEGOVGOAAYSASRGI 188
DB 120 TQSVL-----KMMNAREGALITNMSVYGMGNICQANAYASKGLIFTSVAREVAS 173
QY 189 IGRVMTIAPGLFGTPLTSLPEKVSNFLASQVPEPSRLDPAEYAHVQALILENPEFLNG 248
DB 174 RNRVAVVIAFGMIESDMTILSDKIKKAVLAQIFM-KERGOAQQVADLVFLAGODYILNG 232
QY 249 EVIRIDGAIIRM 259
DB 233 QVTAIDGGLSM 243

RESULT 14
US-09-815-242-13381
Sequence 13381, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815.242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206.848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207.727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242.578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253.625
```

PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13581
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-815-242-13581

Query Match 25.3%; Score 329.5; DB 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 4.5e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLGATATERTLVGASAVLDDLPNSGGE-----AQAKKLGNNCFAPADVTSE 68
DB 10 ITGSSRGIGLALAKFKQAQANIVL-----NSRGAISELLAEFSNIGIKYVPIISGDVSD 65
QY 69 KDVTALALAKGKRGVDVAVNCAGIYASAKTYNLKKQTHLEDFQRLVDVNLKGTENVY 128
DB 66 ADARMTIDQIAELGSDVLIYNNAGI--TODTLMLEK---TEADFEKVLKYNLTGAFNM 119
QY 129 IRLVAGMGNEPQGGGQGVYIINTASVAFEGVGQAAYASAKGIVGCTLPARDLAP 188
DB 120 TQSYL-----KPMKRRREGAIIIMSSVGLMGNTGQANYAASKAGLIGTKSVAREVAS 173
QY 189 IGRVMTIAPGLFSTPLTSLPEKVSNFLASQVFPFSRLDPAEYAHVQAIENPFLNG 248
DB 174 RNIRVNIAPGMISDMTALISDKIKETLAQIPM-KEFGAQEADVLFVFLAGQDYLTG 232
QY 249 EVIRLDGAIRM 259
DB 233 QVIAIDGGLSM 243

RESULT 15
US-09-815-242-10921
Sequence 10921, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10921

LENGTH: 245
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-815-242-10921

Query Match 24.7%; Score 321.5; DB 10; Length 245;
Best Local Similarity 33.7%; Pred. No. 2.4e-21;
Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;

QY 15 ITGASGLGATATERTLVGASAVLDDLPNSGGEAQAKKLGNNCFAPADVTSEKD 70
DB 10 ITGSTRGICQKAVLAFKAGANIVYNGSEITPEQRLELA--ISVKRIGLSGDISDPA 67
QY 71 VQTAIALAKGKRGVDVAVNCAGIYASAKTYNLKKQTHLEDFQRLVDVNLKGTENVY 130
DB 68 AGEMIQATVDQGSIDILVNNAGIT-----NDKILLRMTKEDEFNACIDINLVSTFNM 121
QY 131 EVAGMGNEPQGGGQGVYIINTASVAFEGVGQAAYASAKGIVGCTLPARDLAPIG 190
DB 122 QAVKRMKQ-----RSGRITIMASVSGLMGVGQANYAASKAGVGTAKVAREVAPRG 175
QY 191 INVTIAPGLFSTPLTSLPEKVSNFLASQVFPFSRLDPAEYAHVQAIENPFLNGEV 250
DB 176 ITCNMIAPGFQIOTEMTDVLSKVKYQNMNAQIPLOT-FQVVDVATATLFLAKSPYITGOV 234
QY 251 IRLDGAIRM 259
DB 235 VAVDGGGLVM 243

RESULT 16
US-10-175-696-14
Sequence 14, Application US/10175696
Publication No. US20030092658A1
GENERAL INFORMATION:
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-193001
CURRENT APPLICATION NUMBER: US/10/175,696
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 10/067,668
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/266,140
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/823,901
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/US01/10720
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/193,920
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/862,658
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: PCT/US01/16380
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/205,675
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/882,837
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: PCT/US01/19319
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/211,727
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
US-10-175-696-14

Query Match 24.1%; Score 314; DB 9; Length 237;

TYPE: PRT
ORGANISM: Bacillus megaterium
US-09-479-040-9

Query Match 23.2%; Score 303; DB 9; Length 247;
Best Local Similarity 29.1%; Pred. No. 1.1e-19;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVKGVAVITGASGGLAETAEELVQG-----ASAVIDLDPNSGGEQAOK 53
DB 3 TLGGKVAIVTGGSKGJGAAITRELASNGKVAVAVNNSSESASAIYKEIKDNGEA---- 58
QY 54 LGNNCFAPADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKK-GQHTLE 112
DB 59 -----IAYQADVSVYDQAKHLIETKAAFQGLDILVNNNGI---TRDRFKLGE-----E 106
QY 113 DEQRLVDVNLMTFNVIRLVAGMGQNEPDGQGRVYIINTASVAAFEQVQGAAYSASK 172
DB 107 DMKKVIDVNLHSYNTSALTLELSE---GGR---VINISSIIQAGFGQNTYSAK 160
QY 173 GGIVGMLTPIARDLAPIGIRVMTIAPGLFQTPLLTSLEPKVSNFLASQVFPFSRLDPAE 232
DB 161 AGMLGFTKSLALDELAKTGYVNAICPGFIETEMVAIPEDVRAKIYAKIP-TRRLGHAE 219
QY 233 YAH-LVOATTEPNFNGEVRILDGAIRM 259
DB 220 IARGVYIANDGAYITGOQLNINGGLYM 247

RESULT 20

US-09-773-748-1
Sequence 1, Application US/09773748
Publication No. US20020187537A1
GENERAL INFORMATION:
APPLICANT: Wada, Masaru
TITLE OF INVENTION: Levodione reductase gene and use thereof
FILE REFERENCE: Levodione reductase
CURRENT APPLICATION NUMBER: US/09/773,748
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: EP00101665.8
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 267
TYPE: PRT
ORGANISM: Corynebacterium aquaticum
US-09-773-748-1

Query Match 22.6%; Score 294.5; DB 9; Length 267;
Best Local Similarity 31.8%; Pred. No. 7.4e-19;
Matches 84; Conservative 46; Mismatches 97; Indels 37; Gaps 9;

QY 12 VAVITGASGGLATARLVQGASAVILDLPLNSGGEQAOKKGNMCVAP-----ADVT 66
DB 15 VVLTGGSSGIGRTAVRLAAEGAKLSLVVSSSEGLASRAAVLETAAPDEVLTVYADVS 74
QY 67 SEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKQHTLEDFQRLVDVNLMTGF 126
DB 75 DEAEVAVYVATITRFRIDGFFNNAGIBEQ-----NPFESTFAEFDDVSGVNLRGVF 129
QY 127 -----NVIRLVAGMGQNEPDGQGRVYIINTASVAAFEQVQGAAYSASKGIVGMLPI 182
DB 130 LGELKVKLMR-----EGGS---GMVVTASVGGIRGIGNSGVYAAAHGVVGLTRMS 179
QY 183 ARDLAPIGIRVMTIAPGLFQTPLLTS-----PEKVS-NFLASQVFPFSRLDPAEY 233
DB 180 AVEGRGIRINALAPAIWTPWENSMKOLDPENPKAAEELI---QVNSKRYGAEPI 237
QY 234 AHLVQALLEN--PFLNCEVIRLDG 255
DB 238 AAAYAFLLSDSDASVYVNAIVYIDG 261

RESULT 21
US-10-307-385-6
Sequence 6, Application US/10307385
Publication No. US2003007797A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZUKI, KENZO
TITLE OF INVENTION: XYLIOTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THERE
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/10/307,385
PRIOR FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US/09/363,189
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: JP10-216047
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT
ORGANISM: Gluconobacter oxydans
US-10-307-385-6

Query Match 22.5%; Score 293.5; DB 9; Length 262;
Best Local Similarity 31.6%; Pred. No. 8.9e-19;
Matches 86; Conservative 42; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGGLATARLVQGASAVILDLPLNSG---GEQAOKKGNMCVAP 62
DB 3 KKFNGKCVLTGAGGNNIGATLRLAEGTALALAKRPALEKRAEASVREKGYEABYV 62
QY 63 ADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKQHTLEDFQRLVDVNL 122
DB 63 CVTSEEAIVTGVSDVSDFKIDPLFNNAVGCA-----FAPVDYPSDDFARVLTIVN 117
QY 123 MGFNVIRLVAGMGQNEPDGQGRVYIINTASVAAFEQVQGAAYSASKGIVGMLPI 181
DB 118 TGAFFVLKAVSRQMTQR-----YGRIVMTASVAGVGPNNMAAYGASGAILTLET 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GTPLLTSLEPKVSNFLASQVFPFS 225
DB 171 AALDLAPYIRINALSPGYMGFEMERQVELQAKVGSQYSTDKVVAAQGMISVPR-R 229
QY 226 RUGDPAEVAHLVQALII--ENPFLNGEVRILDG 255
DB 230 RYGDINEITPGVAFLLGDSSPMTGVNPIAG 261

RESULT 22
US-09-802-853-6
Sequence 6, Application US/09802853
Patent No. US20010034049A1
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZUKI, KENZO
TITLE OF INVENTION: XYLIOTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THERE
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/802,853
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 09/363,189
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT

ORGANISM: Gluconobacter oxydans
US-09-802-853-6

Query Match 22.5%; Score 293.5; DB 10; Length 262;
Best Local Similarity 31.6%; Pred. No. 8.9e-19;
Matches 86; Conservative 42; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVGLVAVITGASGLGATFAERLVGOGASAVLLDPNNG---GEAOKKLNCCVFAP 62
DB 3 KFFNGKVCIVTGAAGNIGLALRLAEGRALALDDNNRRLAEKAEISVEKGEARSYV 62
QY 63 ADVTSEKDVCTALALAKGKFGKGRDVAVNCAGIAVASTYMLKKGQTHLEDFORVLDVNL 122
DB 63 CDVTSEAVITGVSVVDFGKIDFLFNNGAYOGA----FAVQDYPSPDDFAVILINV 117
QY 123 MGFNVIRLVAGEM-GONEPDGQGRGVIINTASVAPEGOVGOAAYASAKGIVGWTLP 181
DB 118 TGAHVLEKAVSRQITON-----YGRIVNTASMAVKGPPNMAAGASKGALITLTF 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GTPLTSLPEKVSNFLASQVFPFS 225
DB 171 AALDLAPYRIVNVAISPGYKPGFMERQVELAKVGSQYFSTDPKYVAQOMIGSVPM-R 229
QY 226 RLGDPAEYAHLYQ--ENPELNGEVIARDG 255
DB 230 RYGDINEIPGVAVFLDGDSEFMTGVNLPJAG 261

RESULT 23

US-09-815-242-10126
Sequence 10126, Application US/09815242

Patent No. US20020061569A1
GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815.242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: fastseq for Windows Version 4.0

SEQ ID NO 10126

LENGTH: 244

TYPE: PRF

ORGANISM: Escherichia coli

US-09-815-242-10126

Query Match 22.4%; Score 291.5; DB 10; Length 244;
Best Local Similarity 30.0%; Pred. No. 1.2e-18;
Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;

9 KGLVAVITGASGLGATFAERLVGOGASAVLLDPNNGEAGAKKLGNNCVFAPADVTSE 68

DB 4 EGRKIALVTGASRGIGRAIAETLARGAKVIGTATSENGAQALISDYLGANGKMLNVTDP 63
QY 69 KVOYQTLALAKKFGKGVNDVAVNCAGIAVASTYMLKKGQTHLEDFORVLDVNL 128
DB 64 ASIESVLEKIRAEFGVVDLLVNNAGITRDNLMRKD-----EEMNDIIEITNLSSVRL 117
QY 129 IRLVAGEMONGNEPDGQGRGVIINTASVAPEGOVGOAAYASAKGIVGWTLP 188
DB 118 SKAVMAAMKK-----RHGRITITIGSVYGVGNGNGQANVAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVNTIAPGLFETPLTSLPEKVSNFLASQVFPFSRLGDPAEYAHLYQ--AIIENFPL 246
DB 172 RGTIVVAVAPGLETDMTRALSDDOFAGILACP-AGRLGAGQETANNAVFLASDEAAIYI 230
QY 247 NGEVIRLDGAIRM 259
DB 231 TGETLHVNGMYM 243

RESULT 24

US-09-978-295A-468
Sequence 468, Application US/09978295A

Patent No. US2002015606A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Flivaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavyn, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William J.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630P1C11

CURRENT APPLICATION NUMBER: US/09/978.295A

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      22.3%; Score 290.5; DB 9; Length 270;
Best Local Similarity 32.3%; Pred. No. 1,76-18;
Matches 85; Conservative 43; Mismatches 114; Indels 21; Gaps 8;

QY 1 MAACRSYKGLVAVITGASGLGATERTLVGQASAVLLDLPNSGGEAOKKIGNCVF 60
Db 1 MATGTR-YAGKVVVVTGGGRIGAGIYRAPFNSARVYIDCKDESSGRALDEQL-PEAVF 58
QY 61 APAYTSKDVQZLALAKGKFGYDVAVNCAGIYAVASKTYNNLKGQTHLEDFQVLDV 120
Db 59 ILCDVTGEDDVKTIVSETIRFRGLDCVNNAGHPPPP-----QRPETSAQGRQLLEL 113
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; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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us-09-931-186-23.rapb

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PRIOR APPLICATION NUMBER: 60/085697

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OM protein - protein search, using sw model

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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ALIGNMENTS

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; Sequence 2, Application US/08815225

; Patent No. 6268479

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Yan, Shi Du

; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE

; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING

; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,225

; FILING DATE: 12-MAR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/55209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 261 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-815-225-2

Query Match 99.6%; Score 1299; DB 4; Length 261;

Best Local Similarity 99.6%; Pred. No. 1,1e-135;

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RESULT 2

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; APPLICANT: Yan, Shi Du
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; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS
; NUMBER OF SEQUENCES: 5
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; ADDRESSEE: Cooper & Dunham LLP
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; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,225
; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-815-225-3
```

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Query Match 99.6%; Score 1299; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 1,1e-135;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEQAQKLGNNCF 60
DB 1 MAAACRSYKGLVAVITGGASGLGATAEKLVGOGASAVLLDLPNSGGEQAQKLGNNCF 60
QY 61 APADVSEKDVQOTALAKGKFGKRDVAVNCAAGIAVASKTYNLKKGQTHLEDFORVLDV 120
DB 61 APADVSEKDVQOTALAKGKFGKRDVAVNCAAGIAVASKTYNLKKGQTHLEDFORVLDV 120
QY 121 NLMGFTNVRILVAGENGNEPDGGGQGVYIINTASVAAREGQVGAAYASASGKGIIVGML 180
DB 121 NLMGFTNVRILVAGENGNEPDGGGQGVYIINTASVAAREGQVGAAYASASGKGIIVGML 180
QY 181 PIARDLAPIGIRMTIAPGLFGTFLTSLPEKVSNTLASOVFPSPRLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRMTIAPGLFGTFLTSLPEKVSNTLASOVFPSPRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
DB 241 IENPFLNGEYIRLDGAIRMOP 261
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RESULT 3
US-09-347-878-50
; Sequence 50, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
```

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
;; FILE REFERENCE: 25885-1651
;; CURRENT APPLICATION NUMBER: US/09/347,878C
;; CURRENT FILING DATE: 1999-07-06
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 50
;; LENGTH: 261
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-347-878-50

Query Match 99.6%; Score 1299; DB 4; Length 261;
Best Local Similarity 99.6%; Pred. No. 1.1e-135;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAACRSVKGLVAVITGGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCYF 60
DB 1 MAAACRSVKGLVAVITGGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCYF 60
QY 61 APADVTSEKDVOTATLAKKGRVDVAVNCAGIYASKTYNLKGQTHLEDFQRYLDV 120
DB 61 APADVTSEKDVOTATLAKKGRVDVAVNCAGIYASKTYNLKGQTHLEDFQRYLDV 120
QY 121 NLKGFNVIRLVAGEMQNEPDGQGGQGVIIINTASVAEFEGVQQAAYSASKGIVGM 180
DB 121 NLKGFNVIRLVAGEMQNEPDGQGGQGVIIINTASVAEFEGVQQAAYSASKGIVGM 180
QY 181 PIADLAPIGIRVMTIAPGLFGPTPLTSLPEKYSNFLASQVPPSRIGDPAEYAHLYQAI 240
DB 181 PIADLAPIGIRVMTIAPGLFGPTPLTSLPEKYSNFLASQVPPSRIGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVRILDGAIRMQP 261
DB 241 IENPFLNGEVRILDGAIRMQP 261

RESULT 4
US-08-980-832-41
; Sequence 41, Application US/08980832B
; Patent No. 6291204
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/08/980,832B
; CURRENT FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Flavobacterium sp. R1534
US-08-980-832-41

Query Match 51.2%; Score 667.5; DB 4; Length 388;
Best Local Similarity 55.5%; Pred. No. 1.7e-65;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;
QY 8 VKGLVAVITGGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCYFAPADVTSE 67
DB 143 IEGRVFVVTGAASGLGASARMLAOGAKVYLADL-----AEPKDAPEGAVHAACDYTD 196
QY 68 EKDVTATLAKKGRVDVAVNCAGIYASKTYNLKGQTHLEDFQRYLDVNLKGFNV 127
DB 197 ATAACTATLAKKGRVDVAVNCAGIYASKTYNLKGQTHLEDFQRYLDVNLKGFNV 254
QY 128 VTRLVAGEMQNEPDGQGGQGVIIINTASVAEFEGVQQAAYSASKGIVGM 187
DB 255 MARLAFAEAMARNEPVR-GERGVYIVTASIAAQQDQIGOVAVAAASAGVAGMTLPAROLA 313
QY 188 PIGIVMTIAPGLFGPTPLTSLPEKYSNFLASQVPPSRIGDPAEYAHLYQAI 247

DB 314 RHGIRVMTIAPGLFGPTPLTSLPEKYSNFLASQVPPSRIGDPAEYAHLYQAI 247
QY 248 GEVIRLDGAIRMQP 261
DB 374 GEVIRLDGAIRMQP 387

RESULT 5
US-09-239-052-2
; Sequence 2, Application US/09239052
; Patent No. 6346395
; GENERAL INFORMATION:
; APPLICANT: Holmes, David J.
; APPLICANT: Zhong, Yixi
; APPLICANT: Dedouck, Christine
; APPLICANT: Jaworski, Deborah D.
; APPLICANT: Wang, Min
; APPLICANT: Warren, Richard L.
; APPLICANT: Kosmatka, Anna L.
; APPLICANT: McDevitt, Damien
; APPLICANT: Ingraham, Karen A.
; APPLICANT: Chalker, Allison F.
; APPLICANT: So, Chi Young
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Pearson, Stewart C.
; TITLE OF INVENTION: FabG
; FILE REFERENCE: GM10191
; CURRENT APPLICATION NUMBER: US/09/239,052
; CURRENT FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 25.3%; Score 329.5; DB 4; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.2e-28;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
QY 15 ITGASGLGATAERLVGGASAVLLDLPNSGGE-----AOKKLGNNCYFAPADVTSE 68
DB 10 ITSSSGSIGLAIHAKRAQAGANTYL-----NSRGATSELLAEFSNTGIVYVTSQDVSDF 65
QY 69 KDVTATLAKKGRVDVAVNCAGIYASKTYNLKGQTHLEDFQRYLDVNLKGFNV 128
DB 66 ADAKRMIIDQAIABELGSDVLYNNAGI--TQDTMLKML---TEADEEKLKYNLGAQAFNM 119
QY 129 IRLVAGEMQNEPDGQGGQGVIIINTASVAEFEGVQQAAYSASKGIVGM 188
DB 120 TQSVL-----KPMKFAEATITNMSVVGKNGINQANPAKACGLFTSVAREVAS 173
QY 189 IGRVMTIAPGLFGPTPLTSLPEKYSNFLASQVPPSRIGDPAEYAHLYQAI 247
DB 174 RNRVNVVIAAGMESDMTALISDKINEATLQIPM-KERGOAQVADVLDVFLAQQGYLNG 232
QY 249 EVIRLDGAIRMQP 259
DB 233 QVIAIDGGLSM 243

RESULT 6
US-08-815-225-4
; Sequence 4, Application US/08815225
; Patent No. 6268479
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS

Page 4

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? ZIP: 20037
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/440,856A
? FILING DATE: 15-MAY-1995
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: MILLMAN, ROBERT A.
? REGISTRATION NUMBER: 36,217
? REFERENCE/DOCKET NUMBER: 05463-20001.00
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 887-1517
? TELEFAX: (202) 887-0763
? TELEX: 706141
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 333 amino acids
? type: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? :
? US-08-440-856A-4
?
Query Match      22.9%; Score 298.5; DB 1; Length 333;
Best Local Similarity 32.5%; Pred.No.9.9e-25;
Matches 92; Conservative 46; Mismatches 106; Indels 39; Gaps 5;
QY 6 RSYKGVAVITTSAGASGLGATAERLVGGASAVLLDLPNSGGEAOAKRIGNNCVAPADV 65
   ::::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 50 KREGKVALTGTGARIGALIVRLRYLKHAKVIYIDDDAGELAAALGPHYGVRCDV 109
   ::|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 66 TSEKDVOITALAKRGFRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORYLDVNLMT 125
   :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 110 SVEDEVERVERVAAYGRDLVCNNAgy-LGRÖTRAKSILSPDFAGEFDRLRVNALGA 168
   :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 126 FNVTIRLVAGEMGNENPDGOGRGVITINTSVAFEGGOYAAYSASKGIYGMTLPARD 185
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 169 ALGMKAALAMTOR-----RAGSTISVASVAGVLGGLPHTYSKNAIYGTFNMACE 222
   ::|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 186 LADIGIRVNTIAGLGFLPL-----TSLP-----EKVS 214
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 223 LGAHGIRVNCISPFVGAITPMLINAMFGHDASTADADADIDLDAVPSDQEVERMEEV 282
   :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 215 NFLASQVPPPSRLGDPAEYVAHLVQATIEHPFNGETVIRLDGAI 257
   :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 283 RGLATIKGATLRPRDIAB-RALFLASDSDBRTSGHNLYVGCV 324
   :|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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: TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC-007
: CURRENT APPLICATION NUMBER: US/09/134,001C
: CURRENT FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/064,964
: PRIOR FILING DATE: 1997-11-08
: PRIOR APPLICATION NUMBER: US 60/055,779
: PRIOR FILING DATE: 1997-08-14
: NUMBER OF SEQ ID NOS: 5674
: SEQ ID NO 4512
: LENGTH: 263
: TYPE: PR1
: ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4512

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Query Match 22.6%; Score 295; DB 4; Length 263;
Best Local Similarity 32.3%; Pred. No. 1.7e-24;
Matches 86; Conservative 42; Mismatches 104; Indels 34; Gaps 6;

DB 12 VAVTTGASGLATAERLVGGASAVLLDLPNSGGEQAOKL---GNKCYFAPADYSE 68
11 VAVVGAAGGIGLKAERLFEDGYIALVDENAVAKESAELSKEGGEAVAFKADVSNR 70
QY 69 KDVOYALALAKGFGRDVAVNACIAVAASKTYNKKQOTHTLEDFOEVLDPVNLKGTENV 128
DB 71 DQVEVLNNGVYEHFEDLAVLNNAAGLGMTPF-----ESVTFEFGNVGVNNGVYFWG 124
QY 129 IRLVAGEMGQNEPDGQGRGVIIINTASVAAFEGQVQAAYSASKGGIVGMLPIARDIAP 188
DB 125 IQAAIEQF-----DKIGHGKLIINATSOAGVEGNAGLSYSSTKFAVRKGLQVAAADIAE 179
QY 189 IGRVYTAAGLEFGTPLTSLPEKVSNFLASQVPP-----SRLGDPAEYA 234
DB 180 KNTVNAEAPRGIYETPMKGIARK---LAENNGPMEMGKQFTDQIALKRLKPEDEYA 235
QY 235 HLVAQAI--ENPFNGEVIRLDGAI 258
DB 236 NVVSLAGSDSDYITGQITIVDGNR 261

RESULT 9

US-08-793-035-9
Sequence 9, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Slabas, Antoni R.
APPLICANT: White, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Eldborough, Keiran
APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-793-035-9
Query Match 22.6%; Score 295; DB 3; Length 315;
Best Local Similarity 30.5%; Pred. No. 2.2e-24;
Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

QY 4 ACSRSKGLAVITGGASGLATAERLVGGASAVLLDLPNSGGEA----QAOKLGNNC 58
DB 66 AVPEVSPVYVVTGASRGIGKALISL-GRACGVLYNVARSAAKEEVSQIEAVGGQA 124
QY 59 VFAPADYSEKDQVOTALAKGFRGRDVAVNACIIVASKTNTNKKQHTLEDQRLV 118
DB 125 ITFGDVSKEADYAMKRTAIDAGTIDVYVNNAGITRDITLIRKKSQ-----WDEVI 178
QY 119 DVNLMTGFENVIRLVAGEMGQNEPDGQGRGVIIINTASVAAFEGQVQAAYSASKGGIVGM 178
DB 179 DLNLTGYELCTQAARKIMMK-----RKGRITINIASVGLIGNIGQANYAAKAGVIGF 232
QY 179 TLPIARDLAPRGIYVMTIAGLPGTPLTSLPEKVSNFLASQVPPFRLDPAEYALVQ 238
DB 233 SKTARAGCASRNINNVNVCQFIASDMTARLGEDMERKILGTIPL-GRYQQPDVAGLVE 291
QY 239 AIIENP--FLNGEVIRLDGAI 257
DB 292 FLALSPASVYITGQAFITDGI 313

RESULT 10

US-08-793-035-10
Sequence 10, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Slabas, Antoni R.
APPLICANT: White, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Eldborough, Keiran
APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid

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us-09-931-186-23.ral

Page 6

STRANDEDNESS: single
TOPOLOGY: linear
US-08-793-035-10

Query Match 22.6%; Score 295; DB 3; Length 315;
Best Local Similarity 30.5%; Pred. No. 2.2e-24;
Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

QY 4 ACSVAGIVAVITGASGLGATAEERLVGQASAVLLDLPNSGGEA-----CAKKGNNC 58
DB 66 AVKRESPVAVVAVGASGKIGKATALS-GRAGCKVAVNARSKEAEVSKQLEAVGGA 124
QY 59 VFAPADYSEKDYOTALALAKGFGVDVAVNCAGIYASKTYNKKQTHLEDFORVL 118
DB 125 ITFGDYSKADYEAAMKKTALIDAMGFTIDVYVNNAGITRDTLIRKKSQ-----WDEVY 178
QY 119 DVNLMGFVIRLVAGMGNEPDGQGRVITNTASVAFEGVQAAVYASKSGIVGM 178
DB 179 DLNLTGVFLCTQAAATKIMRK-----RKGRITINIASVVGIGINIGQANTAAKAGVIGF 232
QY 179 TLPIARDLAPIGIRVMTIAPGLFTPLLSLPKVENFLASQVFPFSRLGDPFAVYAHVQ 238
DB 233 SKTARAGCARINIVNVVCPFLIASDWTAKLGEDMEKRLIGTIPL-GRYQGPEDVAGIVE 211
QY 239 AITENP---FLNGEVITLDCAI 257
DB 292 FLALSPASVYITGOAFTIDGI 313

RESULT 11
US-09-363-189B-6
Sequence 6, Application US/09363189B
Patent No. 6242228
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TOMODUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZAKI, KENZO
TITLE OF INVENTION: XYTITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/363, 189B
CURRENT FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PRT
ORGANISM: Gluconobacter oxydans
US-09-363-189B-6

Query Match 22.5%; Score 293.5; DB 4; Length 262;
Best Local Similarity 31.6%; Pred. No. 2.4e-24;
Matches 86; Conservative 42; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVGVLVAVITGASGLGATAEERLVGQASAVLLDLPNSG--GEAQAARKLNNCFAP 62
DB 3 KKNFGKVLVAGAGNIGLATALRLAEGETAIALDLNMRLEAKAESVREKVEARSYV 62
QY 63 ADVYSEKDYOTALALAKGFGVDVAVNCAGIYASKTYNKKQTHLEDFORVLNVL 122
DB 63 CDVYSEAVVITGVSVDVDFGKIDFLFNAGYQGA----FAPVDYPSDFEAVLTINV 117
QY 123 MGFENVIRLVAGEM-GQNEPDGQGRVITNTASVAFEGVQAAVYASKSGIVGTLPL 181
DB 118 TGAHFVLAASRQMTQN-----YGRIVTASAGVKGPPNMAAGASGALIALLET 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GPIPLTSLPEKVSNFLASQVFPFS 225
DB 171 AALDLAPYINIRVNAISPGYMGPGEMMERQVELQAKVQSQFSTDPKVVAAQMGISVPM-R 229
QY 226 RLGDPAEYAHVQAIT--ENPFINGEVITRLDG 255

DB 230 RYGDINEIRPGVAVFILDGDDSSFMGMVNLPIG 261

RESULT 12
US-08-375-962B-13
Sequence 13, Application US/08375962B
Patent No. 5731195
GENERAL INFORMATION:
APPLICANT: STIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
APPLICANT: CRISTER, ERIKSSON, ULF.
TITLE OF INVENTION: Isolated Nucleic Acid Molecule
TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,
TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375, 962B
FILING DATE: 20-January-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258, 418
FILING DATE: 6-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34, 894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]
NAME/KEY: reductase (FABG)
US-08-375-962B-13

Query Match 22.0%; Score 287.5; DB 1; Length 244;
Best Local Similarity 29.6%; Pred. No. 1e-23;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;

QY 9 KGLVAVITGASGLGATAEERLVGQASAVLLDLPNSGGEAQAARKLNNCFAPADYSE 68
DB 4 EGRALVATGASRGIRGAIETLAAIRGKVIIGTATSNGQAISDYLGANGKGLMNVDP 63
QY 69 KDVOITALALAKGFGVDVAVNCAGIYASKTYNKKQTHLEDFORVLNLMGFENV 128
DB 64 ASTESLEKIRAEFGVDVAVNAGITRDNLMRKMD-----EEMNDIETNLSVFFL 117
QY 129 IRLVAGMGNEPDGQGRVITNTASVAFEGVQAAVYASKSGIVGTLPLIARDLAP 188
DB 118 SKAVNRAAMKK-----RGRITITISVYGTMGNGQAAVYAAKALVIGFSKSLAEVAS 171
QY 189 IGIRVMTIAPGLFTPLLSLPKVSNFLASQVFPFSRLGDPFAVYAHVQ--AITENPL 246
DB 172 RGTIVVAVPFGLETMTALSDQDPAIGTAQVP-AGRLGAQOETANAVATLASDEAVYI 230

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QY 189 IGRVMTIAPGLFGTPTLLTSLPEKVSNTLASQVPPSPRLGDPAEYAHVQ--AIENPFL 246
Db 172 RGLTVNVVAVPGFIETDMTRALSDQDAGILAQVP-AGRLGGAQEIANNVAFSLASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
Db 231 TGETLHVNGGMYM 243

RESULT 15
US-08-937-993-13
Sequence 13, Application US/08937993
Patent No. 6399344
GENERAL INFORMATION:
APPLICANT: ERIKSSON, ULF; SIMON, ANDRAS; ROMERT, ANNA
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993
FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6399344ember-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-937-993-13

Query Match 22.0%; Score 287.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 1e-23;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;
QY 9 KGLVAVITGASGIGLATAEERLVGOGASAVLLDIPNSGGGAQAARKIGNCVFAPADYTS 68
Db 4 EKGIALVTGASRGIRALTAETLARQGVIGTATSENGAQAISDYLGANGKGLMLNTDP 63
QY 69 KDVOYATLALAKGKGRVDVAVNCAIGIANASTYINLKKGQHTLDDFORVLDVNLMGTFNV 128

Db 64 ASIESVLEKIRAEFGEVDILVNNAGITDNLIMRKD-----EEMNDIETNLSVFR 117
QY 129 IRLVAGEMQONPPDQGGQGVIIINTASVAEEGVGAQASKGIYGMTLPFIARDIAP 188
Db 118 SKAVYRAMMK-----RGRITIGSVGTGNGNGQANVAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLFGTPTLLTSLPEKVSNTLASQVPPSPRLGDPAEYAHVQ--AIENPFL 246
Db 172 RGLTVNVVAVPGFIETDMTRALSDQDAGILAQVP-AGRLGGAQEIANNVAFSLASDEAYI 230
QY 247 NGEVIRLDGAIRM 259
Db 231 TGETLHVNGGMYM 243

RESULT 16
5229279-7
Patent No. 5229279
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
BIOPOLYMERS
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/556,535
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 67,695
FILING DATE: 29-AUG-1987
SEQ ID NO: 7
LENGTH: 246

Query Match 22.0%; Score 286.5; DB 6; Length 246;
Best Local Similarity 31.9%; Pred. No. 1.3e-23;
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY 12 VAVITGASGIGLATAEERLVGOGASAVLLDIPNSGGE-----AQAKKIGNCVFAPADYTS 67
Db 5 IAYVTGGMGIGTALCOQLAKDGFVYAGCGNSPRREKWLQQRALFEDFASGNAVAD 64
QY 68 EKDVOYATLALAKGKGRVDVAVNCAIGIANASTYINLKKGQHTLDDFORVLDVNLMGTFN 127
Db 65 WDSTKTAEPKVSSEVGEVDVLLNNGI---TDDYFRR---WTRADMNAVIDNTLSIFN 118
QY 128 VIRLVAGEMQONPPDQGGQGVIIINTASVAEEGVGAQASKGIYGMTLPFIARDIAP 187
Db 119 VTQVVIDGMA---DGM--GRIVNISVNGQKGFQGTNNYSTARAGJHGFMALAOEVA 172
QY 188 PIGIRVMTIAPGLFGTPTLLTSLPEKVSNTLASQVPPSPRLGDPAEYAHVQAI--ENPF 245
Db 173 TKGVIYNTVSPGFIATDMKAIRODYLDKIVATIFY-KRLSGPEIATSCMLSSSESGF 231
QY 246 NGEVIRLDGAIRM 259
Db 232 STGADFSLNGGLHM 245

RESULT 17
5512669-4
Patent No. 5512669
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
REDUCTASE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 29-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535

Best Local Similarity 28.7%; Pred. No. 4,6e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY 13 AVTTGGASGLTAERLVGOGASAVLLDLPNSGGEAQA-----KTLGNNCFAPADYTS 67
Db 7 ALTVGASRGIGRSIALQLAEEGYN-VAVNAGSKEKAEEAVEEIKAKGVDSFAIQANVAD 65
QY 68 EKDVOTATLAKGKFGFRVDVAVNCAGIAVASKTYNLKGGQTHLEDFORVLDVNLMTFN 127
Db 66 ADEKAMIKREYVSQFSLDVLVNNAGITRDNLMRKE-----QEMDVIDTNLKGVTN 119
QY 128 VIRLVAGMGONEPDGQGVIIINTASVAEFGVGOAASAKSGIYMTLPIDRLA 187
Db 120 CIOKATPQMLRQ-----RSGAIINLSVVGAVGNPDQANVATKAGVIGLTRSARELA 173
QY 188 PIGIRVMTIAPGLFTPLTSLPEKVSNFLASQVPEPSRLGDPAEYAHLYQAIITEN--PF 245
Db 174 SRGITVAVNAPGFVYSMTALSDLEKQMLTQIPL-ARGQDTDIANTYAFASDKAKY 232
QY 246 LNSEVIRLDGAIRM 259
Db 233 ITGQTIHVNGGMYM 246

RESULT 21
US-09-572-810A-2

; Sequence 2, Application US/09572810A
; Patent No. 6365387
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Fdg
; FILE REFERENCE: GMI0192
; CURRENT APPLICATION NUMBER: US/09/572,810A
; CURRENT FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 09/238,481
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-572-810A-2

Query Match 20.9%; Score 272.5; DB 4; Length 246;
Best Local Similarity 28.7%; Pred. No. 4,6e-22;
Matches 73; Conservative 57; Mismatches 103; Indels 21; Gaps 6;

QY 13 AVTTGGASGLTAERLVGOGASAVLLDLPNSGGEAQA-----KTLGNNCFAPADYTS 67
Db 7 ALTVGASRGIGRSIALQLAEEGYN-VAVNAGSKEKAEEAVEEIKAKGVDSFAIQANVAD 65
QY 68 EKDVOTATLAKGKFGFRVDVAVNCAGIAVASKTYNLKGGQTHLEDFORVLDVNLMTFN 127
Db 66 ADEKAMIKREYVSQFSLDVLVNNAGITRDNLMRKE-----QEMDVIDTNLKGVTN 119
QY 128 VIRLVAGMGONEPDGQGVIIINTASVAEFGVGOAASAKSGIYMTLPIDRLA 187
Db 120 CIOKATPQMLRQ-----RSGAIINLSVVGAVGNPDQANVATKAGVIGLTRSARELA 173
QY 188 PIGIRVMTIAPGLFTPLTSLPEKVSNFLASQVPEPSRLGDPAEYAHLYQAIITEN--PF 245
Db 174 SRGITVAVNAPGFVYSMTALSDLEKQMLTQIPL-ARGQDTDIANTYAFASDKAKY 232
QY 246 LNSEVIRLDGAIRM 259
Db 233 ITGQTIHVNGGMYM 246

RESULT 22
US-09-134-001C-4397
; Sequence 4397, Application US/09134001C

; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4397
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4397

Query Match 20.6%; Score 269; DB 4; Length 231;
Best Local Similarity 33.3%; Pred. No. 1e-21;
Matches 66; Conservative 39; Mismatches 81; Indels 12; Gaps 2;

QY 8 VKGIVAVITGGASGLTAERLVGOGASAVLLDLPNSGGEAQA-----KTLGNNCFAPADYTS 67
Db 5 VKEKAVAVITGGASGLTAERLVGOGASAVLLDLPNSGGEAQA-----KTLGNNCFAPADYTS 64
QY 68 EKDVOTATLAKGKFGFRVDVAVNCAGIAVASKTYNLKGGQTHLEDFORVLDVNLMTFN 127
Db 65 KSNIDMLKRAVIDHGHDIIVNAGSGLSKITD-----YVWQWMTMIDVNTKGLH 118
QY 128 VIRLVAGMGONEPDGQGVIIINTASVAEFGVGOAASAKSGIYMTLPIDRLA 187
Db 119 VLOATLPIYLKQ-----SSGHIINLASVSGEPKTNVATGATAAIIHALQSLEKELA 172
QY 188 PIGIRVMTIAPGLFTPL 205
Db 173 RTGVKVTISISPGWYDTPM 190

RESULT 23
US-09-504-358-14

; Sequence 14, Application US/09504358
; Patent No. 6365376
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; APPLICANT: Brostowicz, Patricia C.
; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATE
; FILE REFERENCE: BC1001 US NA
; CURRENT APPLICATION NUMBER: US/09/504,358
; CURRENT FILING DATE: 2000-02-15
; EARLIER APPLICATION NUMBER: 60/120,702
; EARLIER FILING DATE: 1999-February-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Brevibacterium sp HCU
US-09-504-358-14

Query Match 20.6%; Score 269; DB 4; Length 256;
Best Local Similarity 31.3%; Pred. No. 1.2e-21;
Matches 83; Conservative 41; Mismatches 113; Indels 28; Gaps 9;

QY 10 GLVAVITGGASGLTAERLVGOGASAVLLDLPNSGGEAQA-----KTLGNNCFAPADYTS 66
Db 6 KRAVAVITGGAGMGRIOSELVASEGQAVVVDVNEQGRATDAIRASGVANVYKLDVS 65
QY 67 SEKDVOTATLAKGKFGFRVDVAVNCAGIAVASKTYNLKGGQTHLEDFORVLDVNLMTFN 124
Db 66 DESEVELVVSIDAKRGAIVNLVNNAGVYADK-----PHEIDRDLVLSVDVAG 118

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QY 125 TENVIRLVAGEMQNEPDGQGRGVITINTASVAAPFGQVGOAAYSASKGIYGMPLPIAR 184
DB 119 VEFMTKHCIPYKQ---AGG--GAIYVFASIVGLVSOELTPYHAKAGVAVALTRODAV 172
QY 185 DLAPIGIRVMTIAPGLFETPLTSL----PEKYSNF---LASQVPPSRIGDPAEY--AH 235
DB 173 TYGPSNIRVAVNAAPGILITPLVKELSRGPDLGDTIKLMGAHPL--GAVGTPEEVAAT 231
QY 236 LVQAIENPFLNGEVIRLDGAIRMQ 260
DB 232 LFLASEASFTGAVLPVDGYYTQ 256

RESULT 24
US-09-954-314-14
Sequence 14, Application US/09954314
Patent No. 6465224
GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
APPLICANT: Brzostowicz, Patricia C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/954, 314
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 256
TYPE: PRT
ORGANISM: Brevibacterium sp HCU
US-09-954-314-14

Query Match 20.6%; Score 269; DB 4; Length 256;
Best Local Similarity 31.3%; Pred. No. 1.2e-21;
Matches 83; Conservative 41; Mismatches 113; Indels 28; Gaps 9;
QY 10 GLVAVITGASGLATAEERLVGQASAVLLDLPNSGGEQAQKL---GNNCFAPADYT 66
DB 6 GKVAVITGGAAGRGRISELVASEGAQVAVDVNEQEGRATADAIASAGGVANYMKLDVS 65
QY 67 SEDVQFALALAKGKFERVAVNAGINAVASKTYNKKQOTHTLE--DEQRYLDVNMKG 124
DB 66 DESVEVETVSDIAKRGAIIVLVNMGVGTADK-----PTHEIDRIDLDLVSDVKG 118
QY 125 TENVIRLVAGEMQNEPDGQGRGVITINTASVAAPFGQVGOAAYSASKGIYGMPLPIAR 184
DB 119 VEFMTKHCIPYKQ---AGG--GAIYVFASIVGLVSOELTPYHAKAGVAVALTRODAV 172
QY 185 DLAPIGIRVMTIAPGLFETPLTSL----PEKYSNF---LASQVPPSRIGDPAEY--AH 235
DB 173 TYGPSNIRVAVNAAPGILITPLVKELSRGPDLGDTIKLMGAHPL--GAVGTPEEVAAT 231
QY 236 LVQAIENPFLNGEVIRLDGAIRMQ 260
DB 232 LFLASEASFTGAVLPVDGYYTQ 256

RESULT 25
US-08-858-207A-270
Sequence 270, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gamm, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e
US-08-858-207A-270

Query Match 20.6%; Score 268; DB 4; Length 186;
Best Local Similarity 38.7%; Pred. No. 9.4e-22;
Matches 74; Conservative 23; Mismatches 72; Indels 22; Gaps 5;
QY 15 ITGASGLGLATAEERLVGQASAVLLDLPNSGGE-----AQAKLGNNCFAPADYTS 68
DB 10 ITGSSRGIGLAIHAKFAQGANIVL-----NSRGAISEELAEFSYGIKVPISGDVSDF 65
QY 69 KQVQFALALAKGKFERVAVNAGINAVASKTYNKKQOTHTLEDFQFVLDVNMKGTFNV 128
DB 66 ADKRRITDQAIKELSGVDVLVNAGI--TDTLMKLM---TEADFEKVLKVNLTGAENM 119
QY 129 IRLVAGEMQNEPDGQGRGVITINTASVAAPFGQVGOAAYSASKGIYGMPLPIARDLAP 188
DB 120 TQSVL-----KPMKAKARAGALINSSVGLMGNGINQANVYASKGLIGFTKSVAREVAS 173
QY 189 IGIRVMTIAPG 199
DB 174 RNIIRVAVIAPG 184

Search completed: June 23, 2003, 14:35:45
Job time : 14.1667 secs

Thu Jun 26 06:55:05 2003

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Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:21 ; Search time 39.6667 Seconds
(without alignments)
876.767 Million cell updates/sec

Title: US-09-931-186-23

Perfect score: 1304

Sequence: 1 MAACRSVKGAVITGAS.....ENPLNGEVRIDGAINWQP 261

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : A.Genesec.101002.*

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10: /SIDS2/gcgdata/genesec/genesecp-emb1/AA1989.DAT.*
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23: /SIDS2/gcgdata/genesec/genesecp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	99.6	261	19	AAW71471
2	1146	87.9	260	20	AAV32239
3	1136	87.1	227	20	AAW67934
4	910	69.8	255	22	ABB62988
5	667.5	51.2	388	18	AAW06513
6	364.5	28.0	244	23	ABP28011
7	354	27.1	243	23	ABP27345
8	329.5	25.3	243	19	AAW80670
9	329.5	25.3	243	21	AAW15706
10	329.5	25.3	243	22	AAU37767

11	329.5	25.3	243	22	AAU37988	Streptococcus pneu
12	328.5	25.2	243	22	AAW01032	CPE 35 protein seq
13	327.5	25.1	243	22	ABW54087	Lactococcus lactis
14	321.5	24.7	245	22	AAU55328	Enterococcus faec
15	317	24.3	257	22	AAU28344	Novel human secret
16	314	24.1	237	22	AAW50255	Human dehydrogenas
17	313.5	24.0	248	21	AAV54422	Amino acid sequenc
18	312.5	24.0	241	22	AAW56337	Purative P. abysci
19	312	23.9	237	22	AAU28156	Novel human secret
20	312	23.9	237	22	AAW19928	Human oxaloreducta
21	306.5	23.5	247	22	ABW48892	Listeria monocytog
22	303	23.2	247	21	AAV95746	Bacillus megaterium
23	300.5	23.0	288	22	AAU28296	Novel human secret
24	295	22.6	263	23	ABP39667	Staphylococcus epi
25	295	22.6	315	17	AAW89323	Rape seed beta-ket
26	295	22.6	315	17	AAW89322	Rape seed beta-ket
27	294.5	22.6	267	22	AAW87459	Letrodione reductas
28	294	22.5	262	22	AAW83032	S. epidermidis ope
29	293.5	22.5	262	22	AAW86337	G. suboxydans DSM
30	291.5	22.4	244	21	AAV54421	Amino acid sequenc
31	291.5	22.4	244	22	AAU34533	E. coli cellular p
32	290.5	22.3	270	20	AAV41761	Human PRO474 prote
33	290.5	22.3	270	21	AAW44317	Human PRO474 prote
34	290.5	22.3	270	21	AAW24056	Human PRO474 prote
35	290.5	22.3	270	22	AAU28108	Novel human secret
36	290.5	22.3	279	22	AAU18296	Human endocrine po
37	290.5	22.3	303	23	ABW82624	Heridically activ
38	289.5	22.2	262	21	AAV44578	Xytilol dehydrogen
39	287.5	22.0	246	12	AAW10974	Acetocetyl COA re
40	287.5	22.0	277	21	AAV54415	Secoisolaricresin
41	287	22.0	263	22	AAU58489	Salmonella typhi c
42	286.5	22.0	246	10	AAW94157	Acetyl COA reducta
43	286.5	22.0	246	10	AAW32192	Sequence encoded b
44	286.5	22.0	246	20	AAV3310	Acetocetyl COA re
45	286.5	22.0	246	21	AAV54423	Amino acid sequenc
46	286.5	22.0	246	21	AAW19611	Ralstonia eutropha
47	286.5	22.0	270	21	AAW42558	Human ORF5 ORF232
48	286.5	22.0	329	16	AAW11334	Acetyl COA-reducta
49	284.5	21.8	253	23	ABW54214	Lactococcus lactis
50	283.5	21.7	306	22	AAW81644	S. epidermidis ope
51	283	21.7	280	23	ABW82449	Heridically activ
52	281.5	21.6	273	10	AAW94155	Acetyl COA reducta
53	281.5	21.6	274	23	ABP39585	Staphylococcus epi
54	281	21.5	258	22	AAW32682	C glutamicum prote
55	281	21.5	258	22	AAW9361	Cornebacterium gl
56	280.5	21.5	254	22	AAW49773	Protein with acety
57	278.5	21.4	241	12	AAW10679	Acetocetyl COA re
58	277.5	21.3	242	12	AAW59280	Propionibacterium
59	277	21.2	244	22	AAW81318	Human AFP protein
60	277	21.2	246	14	AAW4761	Acetocetyl COA re
61	276.5	21.2	249	23	ABP39980	Staphylococcus epi
62	275.5	21.1	272	22	AAU37095	Staphylococcus aur
63	275	21.1	285	22	AAW34648	E. coli cellular p
64	274.5	21.1	251	23	AAU34193	Staphylococcus aur
65	274.5	21.1	269	23	ABW52448	Heridically activ
66	274	21.0	206	23	AAW9345	(R)-2-oxanolol deny
67	273.5	21.0	254	22	AAW47522	Pseudomonas aerugi
68	273.5	21.0	286	22	AAU36267	Consensus protein
69	273	20.9	202	23	AAU77210	Staphylococcus aur
70	272.5	20.9	246	21	AAW15707	Staphylococcus aur
71	272.5	20.9	246	22	AAU33965	Staphylococcus aur
72	272.5	20.9	246	22	AAW36530	Staphylococcus aur
73	272.5	20.9	246	22	AAU37210	Staphylococcus aur
74	272.5	20.9	246	22	AAU37507	Staphylococcus aur
75	271.5	20.8	267	21	AAW36959	Chlamydia trachoma
76	270.5	20.7	267	21	AAW35505	Arabidopsis thalia
77	270.5	20.7	308	21	AAW35504	Arabidopsis thalia
78	269.5	20.7	242	22	AAW35381	Haemophilus influe
79	269	20.6	231	23	ABW39552	Staphylococcus epi
80	269	20.6	254	23	ABW48207	Listeria monocytog
81	268.5	20.6	246	22	AAW02195	S. aureus NADPH-de
82	268	20.6	186	19	AAW38474	S. pneumoniae 3-ox
83	267	20.5	247	16	AAW66291	Mycobacterium bovi

FT /note= "alpha helix region A"
 FT 190..196
 FT Region /note= "beta sheet region F"
 FT 204..218
 FT Region /note= "alpha helix region F"
 FT 247..252
 FT Region /note= "beta sheet region G"
 PN W0954347-A2.
 XX 28-OCT-1999.
 PD 19-APR-1999; 99WO-EP02610.
 PF 17-APR-1998; 98US-0082257.
 PR (HORM-) INST HORMON & FORPFLANZUNGSPORSCHUNG GM.
 PA Iwell R, Spiess A, Balvers M, Jaehner D, Hansis C;
 PI WPI: 2000-052699/04.
 DR N-PSDB: AA234663.
 DR Novel differential display reverse transcription PCR method used to
 PT detect genes expressed in mutant tissues
 PS Claim 4; Fig 2; 40pp; English.
 XX This sequence represents murine Alzheimer-associated beta-amyloid
 CC binding protein (ERAB, see AA232239), a novel member of the SCAD
 CC (short chain alcohol dehydrogenase) family of steroid metabolising
 CC and related enzymes. The sequence was deduced from cDNA (see
 CC AA234663) identified using a novel differential display RT-PCR method
 CC for analysis of w/w mouse testis gene products. ERAB is
 CC specifically upregulated in the testicular Leydig cells of w/w
 CC azoospermic mutant mice, suggesting an important role in the
 CC establishment and support of spermatogenesis. The invention also
 CC relates to vectors, host cells, methods for expressing the ERAB
 CC nucleic acid, and antibodies. The nucleic acid and protein are
 CC useful e.g. as markers for testicular development.
 XX

SQ Sequence 260 AA:
 Query Match 87.9%; Score 1146; DB 21; Length 260;
 Best Local Similarity 87.6%; Pred. No. 1,2e-103;
 Matches 226; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 4 ACRSVKGLVAVITGASGIGLTAERLVGQASAVLDDLPSNGGGAQKKIGNNCFAPA 63
 DB 3 AVRSVKGVLAVVTGASGIGLTAERLVGQASAVLDDLPSNGGGAQKKIGNNCFAPA 62
 QY 64 DVTSEKDVOTALALAKKFGKGRVDVAVNCAGIVASAKTYNKKGQHTLEDFQRYLDVNM 123
 DB 63 NTSSEKIOALTLAKKFKGRIDVAVNCAGIVAKTYHKKNKHTLEDFQRYLDVNM 122
 QY 124 GFENVIRLVAGEMGQNEPDQGRVINTASVAAPEGVGQAAVSASKGGIVGKTLPIA 183
 DB 123 GFENVIRLVAGEMGQNEPDQGRVINTASVAAPEGVGQAAVSASKGGIVGKTLPIA 182
 QY 184 RDLAPGIRVMTIAPGLFGTPLTSLPEKVSNNFLASOVFFPSRLDPAEVAHLVOATLEN 243
 DB 183 RDLAPGIRVMTIAPGLFGTPLTSLPEKVSNNFLASOVFFPSRLDPAEVAHLVOATLEN 242
 QY 244 PFLNGEVIRLDGAIRMP 261
 DB 243 PFLNGEVIRLDGAIRMP 260

RESULT 3
 AAM67934
 ID AAM67934 standard; Protein; 227 AA.
 XX
 AC AAM67934;

XX 25-MAR-1999 (first entry)
 DT Fragment of human secreted protein encoded by gene 8.
 XX
 DE Human; secreted protein; fusion protein; gene therapy; protein therapy;
 XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW development; abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 OS
 PN W09842738-A1.
 PD 01-OCT-1998.
 PF 19-MAR-1998; 98WO-US05311.
 XX 30-MAY-1997; 97US-0050937.
 XX 21-MAR-1997; 97US-0041276.
 PR 21-MAR-1997; 97US-0041276.
 PR 21-MAR-1997; 97US-0041281.
 PR 21-MAR-1997; 97US-0042344.
 PR 30-MAY-1997; 97US-0048069.
 PR 30-MAY-1997; 97US-0048094.
 PR 30-MAY-1997; 97US-0048095.
 PR 30-MAY-1997; 97US-0048096.
 PR 30-MAY-1997; 97US-0048099.
 PR 30-MAY-1997; 97US-0048131.
 PR 30-MAY-1997; 97US-0048135.
 PR 30-MAY-1997; 97US-0048154.
 PR 30-MAY-1997; 97US-0048160.
 PR 30-MAY-1997; 97US-0048186.
 PR 30-MAY-1997; 97US-0048187.
 PR 30-MAY-1997; 97US-0048188.
 PR 30-MAY-1997; 97US-0048350.
 PR 30-MAY-1997; 97US-0048351.
 PR 30-MAY-1997; 97US-0048352.
 PR 30-MAY-1997; 97US-0048355.
 PR 05-AUG-1997; 97US-0054804.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
 PI Greene JM, Hu JS, Lalleur DW, Moore PA, NI J, Olsen HS;
 PI Rosen CA, Ruben SM, Shi Y, Young P;
 XX WPI: 1999-070066/06.
 DR N-PSDB: AAX00618.
 XX New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Disclosure; Page 11; 385pp; English.
 XX This sequence represents a fragment of a secreted human protein encoded
 CC by the nucleic acid molecule detailed in the descriptor line. The gene
 CC can be used to generate fusion proteins by linking to the gene to a
 CC human immunoglobulin Fc portion (e.g. AAX00602) for increasing the
 CC stability of the fused protein as compared to the human protein only.
 CC The invention relates to 87 novel genes and their fragments (nucleic
 CC acid sequences: AAX00611-X00724; amino acid sequences AAM67807-W68004)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 87
 CC polynucleotides, based on which tissues they are most highly expressed in

Query Match 51.2%; Score 667.5; DB 18; Length 388;
 Best Local Similarity 55.5%; Pred. No. 1,1e-56;
 Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGIIVITGASGLGIATIERLYVGQASAVLIDLPSNGSGAQAQKLGNNCVAPADVTS 67
 DB 143 IEGRFVVTGAAASGLGAASAMLAQCGAKVLAIDL-----AEKDKAPEGAVHACVTD 196
 QY 68 EKDVTALALAKGFGADVAVNCAGIAVASKTYNLTGQTHLEDFQRLVDVNLMTEN 127
 DB 197 ATAAQTALATLDRGLDGLVNCAGIAPAPERM--LGRDGHGLDSFAPRAVTTINLSFEN 254
 QY 128 VIRLVAGEMGQNEPDGQGRGVITINTASVAAFEGVQQAAYSASKSGIVGMLPIARDLA 187
 DB 255 MARLAELMARNEPVR-GERGVIVNTASIAAQDQIGVAVYAAASKAGVAGMTLPMARDLA 313
 QY 188 PIGIRVMTIAPGLGTPLTSLPEKVSNTLASQVFPFSRLGDPAEVHLVQALLENPFNL 247
 DB 314 RHGIRVMTIAPGIRTPMLBGLPDQVDSLGAAYFPFSRLGSEVYALHLHITANPMLN 373
 QY 248 GEVIRLDGAIKMQP 261
 DB 374 GEVIRLDGALRMAP 387

RESULT 6

ABP28011 standard; Protein: 244 AA.

ABP28011;

02-JUL-2002 (first entry)

Streptococcus polypeptide SEQ ID NO 5198.

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 group A streptococcus; Streptococcus pyogenes; antibacterial;
 antiinflammatory; infection; vaccine; meningitis; gene therapy.

Streptococcus agalactiae.

WO200234771-A2.

02-MAY-2002.

29-OCT-2001; 2001WO-GB04789.

27-OCT-2000; 2000GB-0026333.

24-NOV-2000; 2000GB-0026727.

07-MAR-2001; 2001GB-0005640.

(CHIR-) CHIRON SPA.

(GENO-) INST GENOMIC RES.

Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

Tetella H;

WPI; 2002-352536/38.

N-PSDB; ABN68642.

Claim 1; Page 3863; 4525pp; English.

The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5463 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for

the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I) may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.

Sequence 244 AA;

Query Match 28.0%; Score 364.5; DB 23; Length 244;
 Best Local Similarity 36.5%; Pred. No. 2.4e-27;
 Matches 92; Conservative 38; Mismatches 99; Indels 23; Gaps 5;

QY 15 ITTGASGLGIATIERLYVGQASAVLIDLPSNGS-----AQAKKGNNCVAPADVTS 68
 DB 10 ITGSSRGIGLAIHQAQAGANIVL---NGRSEISEDILAEFADYGAVIAISGVSSF 65
 QY 69 KDVOFTALALAKGFGADVAVNCAGIAVASKTYNLTGQTHLEDFQRLVDVNLMTFNV 128
 DB 66 EDANRMKKEIASLGSVDVLYNNAGIT-----NDKMLKMTVEDESVLKITLNGAFNM 119
 QY 129 IRVLVAGEMGQNEPDGQGRGVITINTASVAAFEGVQQAAYSASKSGIVGMLPIARDLP 188
 DB 120 TQSVL-----KMTKAROGALINISSVGLTGNVQAYVAAASKGLIGFTSVAREVA 173
 QY 189 IGIRVMTIAPGLGTPLTSLPEKVSNTLASQVFPFSRLGDPAEVHLVQALLENPFNL 248
 DB 174 RGIIRVMTIAPGLFTESDMTIVIPKMEAILAQIPM-KRIGKGEVQAVSFLAEQRYLNG 232
 QY 249 EVIRLDGAIKMQ 260
 DB 233 QVIAIDGQMTMQ 244

RESULT 7

ABP27345 standard; Protein: 243 AA.

ABP27345;

02-JUL-2002 (first entry)

Streptococcus polypeptide SEQ ID NO 3866.

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 group A streptococcus; Streptococcus pyogenes; antibacterial;
 antiinflammatory; infection; vaccine; meningitis; gene therapy.

Streptococcus pyogenes.

WO200234771-A2.

02-MAY-2002.

29-OCT-2001; 2001WO-GB04789.

27-OCT-2000; 2000GB-0026333.

24-NOV-2000; 2000GB-0026727.

07-MAR-2001; 2001GB-0005640.

(CHIR-) CHIRON SPA.

(GENO-) INST GENOMIC RES.

Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

Tetella H;

WPI; 2002-352536/38.

N-PSDB; ABN67976

XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX
 PS Claim 1: Page 3542; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have anti-bacterial and anti-inflammatory
 CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
 CC antibodies that bind (1) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a
 CC biological sample. (1) is used to determine whether a compound binds to
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (1) may be used to recombinantly produce (1) and may be
 CC used in gene therapy. Antibodies to (1) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 CC
 XX
 SQ Sequence 243 AA;
 Query Match 27.1%; Score 354; DB 23; Length 243;
 Best Local Similarity 35.4%; Pred. No. 2.5e-26;
 Matches 92; Conservative 42; Mismatches 100; Indels 26; Gaps 6;
 QY 8 VKGIYAVITGGASGLGATAEALVAGGASAVLDDPNSGGEAQAARL-----GNNCVF 60
 DB 3 IKGNI-FTTGSTRIGLAMAHOEASLEANIYL-----NGSAISEELVASFDTGYGVYVT 56
 QY 61 APADVTSEKDYOTALALAKKFRGVDAVAVNCAGIYAVASKTYNKKGGOTHTLEDFORYLDV 120
 DB 57 ISGVSESEAKRMYNAIESLSGLDIVLVNNAIGT-----NDLIMKMEDEPFEVRLKI 110
 QY 121 NLMGTFYIRLYVAEMQNEPDGOGGVIIINTSVAFAGFGVGOQAAYASKSGIVMTL 180
 DB 111 NLTAFFMTQSVL-----KPMIKARQALINSSVGLTGNIGQANYPAASKAGMTGFTX 164
 QY 181 PIARDLAPIGIRVMTIAPGLEFGLPLTSLPEKYSNFTLASOVPPPSRLGDPAEVAHLVQAI 240
 DB 165 SVAREVAARNICVNAIAPGFIESDMTGVLPEKMQEQLISQIPM-KRIGKAQEVANHLASFL 223
 QY 241 IENPFLNGEVIRLDGAIKRMQ 260
 DB 224 VEQDTITGVYALADGSMTQ 243
 Db
 RESULT 8
 AAM80670
 ID AAM80670 standard; Protein: 243 AA.
 XX
 AC AAM80670;
 XX
 DT 24-DEC-1998 (first entry)
 XX
 DE S. pneumoniae fatty acid biosynthesis protein.
 XX
 KM Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
 KM virulence; antibody; infection; detection; treatment; hypothetical;
 KM cell wall biosynthetic; external target; minimal gene set protein.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO9826072-A1.
 XX
 PD 18-JUN-1998.
 XX
 PF 09-DEC-1997; 97WO-US22578.

XX
 PR 13-DEC-1996; 96US-0036281.
 XX
 PA (ELL) LITLY & CO ELI.
 XX
 PI Balz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR,
 PI Mills BJ, Norris FH, Peery RB, Rokey PK, Rostek PR,
 PI Skarud PL, Smith MC, Solenberg PJ, Treadway PJ;
 PI Young Bellido ML;
 XX
 DR WPI; 1998-348529/30.
 XX
 XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
 PT for evaluating gene expression, and identification of virulence
 PT genes
 XX
 PS Claim 3: Page 270; 333pp; English.
 XX
 CC This sequence represents a S. pneumoniae fatty acid biosynthesis
 CC protein. The invention provides DNA sequences (AA65201 to AA65304)
 CC from the Streptococcus pneumoniae genome and corresponding protein
 CC sequences (AAM80605 to AAM80728). The protein sequences are classified as
 CC hypothetical, cell wall biosynthetic, external target, or minimal gene
 CC set proteins. A recombinant host containing a vector comprising any of
 CC the above nucleic acids can be used for the recombinant expression of the
 CC proteins. The invention also provides a DNA chip having arrayed on it at
 CC least 15 base pair fragment of any one or more of these DNA sequences.
 CC The DNA chip can be used methods for evaluating gene expression in S.
 CC pneumoniae and for identifying virulence genes in S. pneumoniae.
 CC Antibodies that selectively bind to the above proteins or peptide
 CC fragments can be used to treat S. pneumoniae infection. The antibodies
 CC can also be used to detect S. pneumoniae cells.
 CC
 XX
 SQ Sequence 243 AA;
 Query Match 25.3%; Score 329.5; DB 19; Length 243;
 Best Local Similarity 35.1%; Pred. No. 6.1e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
 QY 15 ITGGASGLGATAEALVAGGASAVLDDPNSGGE-----AQAKKIGNNCYFAPADVTSE 68
 DB 10 ITGSSSGIGLAIHAKRQAGANIVL-----NGSAISEELAFSNGIKYVPLISDVSDF 65
 QY 69 KDQVOTALALAKKFRGVDAVAVNCAGIYAVASKTYNKKGGOTHTLEDFORYLDVNLGTRV 128
 DB 66 ADAKRMIDDAIELGSDVDLVNNAIGT-----TEADFEKLYKYNLGAERFM 119
 QY 129 IRLVAGEMQNEPDGOGGVIIINTSVAFAGFGVGOQAAYASKSGIVMTLPIARDLAP 188
 DB 120 TQSVL-----KPMKAREGALINSSVGLMGNIGQANYPAASKGLIGFTSVAREVAS 173
 QY 189 IGIRVMTIAPGLEFGLPLTSLPEKYSNFTLASOVPPPSRLGDPAETIAHLVQAIENPFLNG 248
 DB 174 RNIRVNVIAIPGMIESDMTALISDKIKETIAQIPM-KEFGQAQEVADLVFLAGODYILTG 232
 QY 249 EVIRLDGAIKRM 259
 DB 233 QVTAIDGGLSM 243
 Db
 RESULT 9
 AAB15706
 ID AAB15706 standard; Protein: 243 AA.
 XX
 AC AAB15706;
 XX
 DT 07-DEC-2000 (first entry)
 XX
 DE Streptococcus pneumoniae Fabg polypeptide.
 XX
 KM Streptococcus pneumoniae; Fabg; 3-oxoacyl-acyl carrier protein reductase;
 KM antibacterial; cytostatic; antitumor; cancer; gastric ulcer; gastritis;
 KM Helicobacter pylori infection; microbial infection.

XX Streptococcus pneumoniae.
 OS
 XX WO200044885-A1.
 PN
 XX 03-AUG-2000.
 PD
 XX 19-JAN-2000; 2000MO-US01131.
 PF
 XX 27-JAN-1999; 99US-0239052.
 PR
 XX (SMK) SMITHKLINE BEECHAM CORP.
 PA
 XX Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DJ, Wang M;
 PI Warren RL, Kosmatka AL, Mcdevitt D, Ingraham KA, Chalker AF;
 PI So CY, Wallis NG, Pearson SC;
 XX WPI; 2000-482971/42.
 DR N-PSDB; AAA/4684.
 XX
 XX FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
 PT treat microbial diseases, identify agonists and antagonists for
 PT treating microbial infections and to detect diseases associated with
 PT microbial infections -
 PT
 XX Claim 1; Page 3; 40pp; English.
 PS
 XX The present sequence is a FabG (2-oxoacyl-acyl carrier protein
 CC reductase) polypeptide. A full length FabG gene was isolated from a
 CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
 CC polynucleotides and polypeptides are used for detection and treatment of
 CC microbial diseases. They may also be used to identify antagonists and
 CC agonists which can then be used to treat microbial diseases. Compounds
 CC that interfere with the initial physical interaction between a pathogen
 CC and a host have been identified. The compounds are able to prevent the
 CC adhesion of bacteria to mammalian extracellular proteins in wounds,
 CC prevent adhesion between mammalian extracellular proteins and bacterial
 CC FabG proteins which mediate tissue damage and/or to block normal
 CC progression of pathogenesis in infections mediated by implantation of
 CC in-dwelling devices or other surgical techniques. The FabG
 CC polypeptides, polynucleotides, antagonists and agonists are especially
 CC useful in the treatment of Helicobacter pylori infection. They may be
 CC used to decrease H. pylori-induced cancers and to prevent, inhibit
 CC and/or cure gastric ulcers and gastritis.
 CC
 XX
 XX Sequence 243 AA;
 SQ
 Query Match 25.3%; Score 329.5; DB 21; Length 243;
 Best Local Similarity 35.1%; Pred. No. 6.1e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

AAU37767
 ID AU37767 standard; Protein; 243 AA.
 XX
 XX AC AU37767;
 XX
 XX 14-FEB-2002 (first entry)
 DT
 XX Streptococcus pneumoniae cellular proliferation protein #196.
 DE
 XX Antisense: prokaryotic cellular proliferation protein;
 XX antibiotic; antibacterial; drug design.
 KM
 XX Streptococcus pneumoniae.
 OS
 XX WO200170955-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 21-MAR-2001; 2001WO-US09180.
 PF
 XX 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207127P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 XX (ELIT) ELITRA PHARM INC.
 PA
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PI WPI; 2001-611495/70.
 DR N-PSDB; AAS55626.
 DR
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PT
 XX
 XX Example 3; Seq ID No 13360; 511pp; English.
 PS
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pot_sequences.
 CC
 XX
 XX Sequence 243 AA;
 SQ
 Query Match 25.3%; Score 329.5; DB 22; Length 243;
 Best Local Similarity 35.1%; Pred. No. 6.1e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

Db 66 ADAKRMIDQALAEISVDVLYNNAGI--TQDTLMKMK-----TEADFEKVLKYNLTGAFNM 119
 QY 129 IRLVAGEGQNEPDGQGRGVYINTASVAFEGVQQAAYSASKGIVGMLPIARDLAP 188
 Db 120 TQSVL-----KPMKAREGAIIMSSVYGLMGNIGQANYAASKAGLIGFTKSVAREVAS 173
 QY 189 IGIRVMTAPGLFGPTLTSLEPKVSNFLASQVFPSPRLGDPAEYAHVQAIIENPFLNG 248
 Db 174 RNIRNVYIAPGKIESDMTRAILSDKIKENTLAQIRM-KERFGAEQVADLTVPFLAGQDYLTG 232
 QY 249 EVIRLDGAI RM 259
 Db 233 QVIAIDGGLSM 243
 RESULT 11
 AAU37988 standard; Protein; 243 AA.
 AC AAU37988;
 XX 14-FEB-2002 (first entry)
 DT Streptococcus pneumoniae cellular proliferation protein #417.
 DE Streptococcus pneumoniae cellular proliferation protein;
 XX Antibiotic; prokaryotic cellular proliferation protein;
 KM antibiotic; antibacterial; drug design.
 XX Streptococcus pneumoniae.
 OS
 XX MO200170955-A2.
 PN 27-SEP-2001.
 PD 21-MAR-2001; 2001MO-US09180.
 PF 21-MAR-2000; 2000US-191078P.
 XX 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 XX 23-OCT-2000; 2000US-242378P.
 PR 27-NOV-2000; 2000US-253623P.
 PR 22-DEC-2000; 2000US-257931P.
 XX 16-FEB-2001; 2001US-269308P.
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PI WPI: 2001-611495/70.
 DR N-PSDB; AAS55847.
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 13581; 511bp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Enterococcus faecalis. The
 CC pneumoniae, Pseudomonas aeruginosa and, Salmonella typhi, Klebsiella
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp://ipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 243 AA;
 Query Match 25.3%; Score 329.5; DB 22; Length 243;
 Best Local Similarity 35.1%; Pred. No. 6, 1e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
 QY 15 ITGASGIGLATPBERLVGQASAVLLDLPNSGGE-----AQAKKLNQVFPADYTS 68
 Db 10 ITGSSRGIGLAIARKEFAQAGANIYL---NSRGAISELLAEFSNVIKYPVTSIGDVSD 65
 QY 69 KDVOFALALAKGFGVDVAVNCAGIAVASKTYNLKKRGQTHLEDFOVLVDVNLMTGFNV 128
 Db 66 ADAKRMIDQALAEISVDVLYNNAGI--TQDTLMKMK-----TEADFEKVLKYNLTGAFNM 119
 QY 129 IRLVAGEGQNEPDGQGRGVYINTASVAFEGVQQAAYSASKGIVGMLPIARDLAP 188
 Db 120 TQSVL-----KPMKAREGAIIMSSVYGLMGNIGQANYAASKAGLIGFTKSVAREVAS 173
 QY 189 IGIRVMTAPGLFGPTLTSLEPKVSNFLASQVFPSPRLGDPAEYAHVQAIIENPFLNG 248
 Db 174 RNIRNVYIAPGKIESDMTRAILSDKIKENTLAQIRM-KERFGAEQVADLTVPFLAGQDYLTG 232
 QY 249 EVIRLDGAI RM 259
 Db 233 QVIAIDGGLSM 243
 RESULT 12
 AAU01032 standard; Protein; 243 AA.
 ID AAU01032
 AC AAU01032;
 XX 02-OCT-2001 (first entry)
 DT CFE 35 protein sequence.
 XX
 DE Antibacterial; vaccine; gene therapy; bacterial cell wall viability;
 KM CFE; CEG; Conserved Essential Gene; bacterial infection;
 KM antisense therapy; antibiotic resistance.
 XX Streptococcus pneumoniae.
 OS
 XX MO200149721-A2.
 PN 12-JUL-2001.
 PD 29-DEC-2000; 2000MO-US35604.
 PF 30-DEC-1999; 99US-0174089.
 XX
 PA (BRIN) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Bruccoleri RE;
 PI Thanassi JA;
 PI WPI: 2001-496721/54.
 DR N-PSDB; AAH90731.
 XX
 CC Nucleic acids encoding conserved essential genes involved in bacterial
 CC replication which are potential targets for the treatment of antibiotic
 CC resistant bacterial infections -
 XX
 PS Claim 27; Page 273; 380pp; English.
 XX
 CC The present invention relates to nucleic acids (AAH90701-AAH90918)
 CC encoding polypeptides (AAU01002-AAU01114), which are essential for the
 CC viability of a bacterial cell wall. The acronym CFE stands for "Conserved
 CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic

XX Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GU;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS3187.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 10921; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcr_sequences.
 CC
 XX Sequence 245 AA;
 SQ
 Query Match 24.7%; Score 321.5; DB 22; Length 245;
 Best Local Similarity 33.7%; Pred. No. 3.8e-23;
 Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;
 QY 15 ITGGASGGLTARILVGGASAVLTD---LPNSGGPAQKKLGNVCVPAPADVSEKD 70
 DB 10 ITGSTRIGKAVLAFAKESANITLNGRSETTPQRQRIEA--FGVACIGSDISPDFA 67
 QY 71 VQTALALAKGFRGADVAVNACIJAASVSKTYLNKGGTHLEDFORVLDVNMKTENVIR 130
 DB 68 AGEMIQATVDQIGSDILVNNAGIT-----NDKLLRMTEDEFNACIDILVGFNNMQ 121
 QY 131 LVAGMGONEPDQGGRGVITNTASVAFEGVQGANVSAKSGEIVGMTLPIARDLAPIG 190
 DB 122 QAVKRMKQ-----RSRRITMASVSGMLGNVQGANVSAKSGEIVGMTLPIARDLAPIG 175
 QY 191 IRVMTIAGLEGTPLTSLPERKVSNTLASQVPPFSRLGDPFAEVAHLVQATITENPLNGEV 250
 DB 176 ITCNAIAGCFIQIETDVLSEKVKTKQMAQIPLOT-FQGVEDVAATAFILAKSPYITGV 234
 QY 251 IRLDGAIRM 259
 DB 235 VAVDGGGLVAV 243
 Db
 RESULT 15
 AAU28344
 ID AAU28344 standard; Protein; 257 AA.
 XX
 AC AAU28344;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secretory protein, Seq ID No 701.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 OS
 OS Homo sapiens.
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001MO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-065363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX WPI; 2001-589934/66.
 DR N-PSDB; AAS43244.
 DR
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Example 2; SEQ ID No 701; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 XX
 SQ Sequence 257 AA;
 XX
 Query Match 24.3%; Score 317; DB 22; Length 257;
 Best Local Similarity 31.5%; Pred. No. 1.1e-22;

KM (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;
 KM beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;
 KM polybeta-hydroxy fatty acid biosynthesis; optically active;
 KM 4-halo-3-hydroxybutyric acid ester.

OS Bacillus subtilis.

PN EP95375-A2.

PD 10-NOV-1999.

PF 10-MAY-1999; 99EP-0109403.

PR 08-MAY-1998; 98JP-0126507.

PR 21-OCT-1998; 98JP-0300178.

PR 05-APR-1999; 99JP-0098205.

PA (DAICEL CHEM IND LTD.

PI Yamamoto H;

DR WPI, 2000-118183/11.

DR N-PSDB; AA245749.

PT Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -

PS Claim 6; Page 19-20; 34pp; English.

XX The present sequence represents a beta-ketoacyl-ACP reductase protein
 CC of Bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme constitutes
 CC a type II fatty acid synthetase. The enzyme has an extremely high
 CC reducing activity and stereoselectivity towards 4-chloroacetoacetic
 CC acid ester. The specification describes a method for producing a
 CC (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
 CC asymmetrically reducing 4-halo-acetoacetic acid ester or its
 CC derivative with beta-ketoacyl-acyl carrier protein reductase
 CC constituting type II fatty acid synthase, or acetoacetyl-CoA
 CC reductase constituting the polybeta-hydroxy fatty acid biosynthesis
 CC system. The novel method is used to produce optically active
 CC 4-halo-3-hydroxybutyric acid ester, with a high purity.

XX Sequence 248 AA;

Query Match 24.0%; Score 313.5; DB 21; Length 248;

Best Local Similarity 29.7%; Pred. NO. 2.3e-22;

Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;

QY 13 AVITGGSGTGLATFAERLVGOGASAVLLDLPNSGGEAQA-----KTIQNNQVFPADY 65

DB 9 AITTGASRGIGRSLALALAKSGANV---VYSGNPAKANEVDLRKSGRAIAKADY 65

QY 66 TSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKQTHLEDFQRLVDVLMQT 125

DB 66 SNEDVQNMIRKETLSVFSTIDILVNNAGITRDLIMRKE-----DEMDVIVINILKGV 119

QY 126 FNYTRLVAGEMGNEPPOGGRGVITNTASVAFEGOVQAAYASAKSGIVGWTLDIARD 185

DB 120 FNCIKAVTRQMKO-----RSGRIIVSSIVGSGNPGQANVAAKAGVIGLTRSSAKE 173

QY 186 LAPIGIRVMTIAGLEFETPLTSLPEKVSNFLASQVFPFSRLQDPAEYAHLYQAITEN-- 243

DB 174 LASRNTIVNAIARGFISTDMTKLAKVDQDEMLKQIPL-ARFGSPDSVSSVYFLASEGA 232

QY 244 PFLNGEVIRLDGAIARM 259

DB 233 RYMGQPLHIDGKVM 248

RESULT 18

AA96397

XX ID AAB96397 standard; Protein: 241 AA.

XX AC AAB96397;

XX 29-OCT-2001 (first entry)
 DX Putative P. abyssi dehydrogenase #8.
 DE
 XX
 KM Hyperthermophilic archaeon; hyperthermophilic protein.

OS Pyrococcus abyssi.

PN FR2792651-A1.

PD 27-OCT-2000.

PF 21-APR-1999; 99FR-0005034.

PR 21-APR-1999; 99FR-0005034.

PA (CNRS) CNRS CENT NAT RECH SCI.

PI (IFREMER) IFREMER INST FR RECH EXPL MER.

DR Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

DR Querellou J, Weissenbach J, Saurin W, Helling R;

DR WPI, 2001-126236/14.

PT New nucleotide sequences isolated from Pyrococcus abyssi encode

PS proteins useful in industry -

PS Claim 7; Pages 1087-1088; 1657pp; French.

XX The present invention relates to the genomic sequence of Pyrococcus
 CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is
 CC a hyperthermophilic archaeon, which is isolated from deep-sea
 CC hydrothermal vents. The present sequence is one such P. abyssi protein.
 CC The proteins of the present invention have various potential industrial
 CC uses, since the proteins are stable at very high temperatures, some up to
 CC 110 degrees centigrade.
 CC Note: This patent is in the same patent family as WO200065062, which
 CC contains additional sequences as shown in AAB99132-AAB99143,
 CC AAH75903-AAH75920 and AAG66436.

XX Sequence 241 AA;

Query Match 24.0%; Score 312.5; DB 22; Length 241;

Best Local Similarity 34.1%; Pred. NO. 2.8e-22;

Matches 87; Conservative 47; Mismatches 92; Indels 29; Gaps 7;

QY 8 VGLVAVITGGSGTGLATFAERLVGOGASAVLLDLPNSGGEAQA-----VF 60

DB 4 LKGRVALLITGASRGIGRAIAIEIAKRGVNVVINTRSN---DEEAKKIEELCRQYGVETLL 60

QY 61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKQTHLEDFQRLVDV 120

DB 61 VKADVSNEEVEAEWKVYIDKFRGIDILINNAGI--LQKT---KDPLEVDDEEDRVISV 115

QY 121 NLMGFNYTRLVAGEMGNEPPOGGRGVITNTASVAFEGOVQAAYASAKSGIVGWTLDIARD 180

DB 116 NIKGAFITYQEVLRM-----KRGRIYNASIAKDGQVGPVPHAAKSGGLIALTF 166

QY 181 PIARDLAPIGIRVMTIAGLEFETPLTSLPEKVSNFLASQVFPFSRLQDPAEYAHLYQAIT 240

DB 167 NIAERLAP-NILVNAVAAGPVDWTLSEMEK-----MKTKSLTGDIAPKEPVAHAAYFL 221

QY 241 IENPFLNGEVIRLDG 255

DB 222 LENDHITGEVDVNG 236

RESULT 19

AAU28156

XX ID AAU28156 standard; Protein: 237 AA.

XX AC AAU28156;

18-DEC-2001 (first entry)
Novel human secretory protein, Seq ID No 325.
Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; infertility; analgesic; pain; antigen.
Homo sapiens.
W020016689-A2.
13-SEP-2001.
05-MAR-2001; 2001WO-US04942.
07-MAR-2000; 2000US-0519705.
19-MAY-2000; 2000US-0574454.
17-JUN-2000; 2000US-0596193.
14-JUL-2000; 2000US-0616647.
19-SEP-2000; 2000US-0665363.
20-OCT-2000; 2000US-0693267.
(HYSEQ-) HYSEQ INC.
Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P, Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J; N-PSDB; AAS45056.
Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders -
Example 4; SEQ ID No 325; 107pp; English.
The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biocycles or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals provides

[illegible]

DR N-PSDB: AAA89187.
 XX
 PT New human oxidoreductase proteins useful for diagnosing, treating or
 PT preventing proliferative, neurological, genetic, smooth muscle,
 PT autoimmune or inflammatory disorders associated with abnormal
 PT expression of oxidoreductase proteins
 XX
 PS Claim 1(a); Page 83; 95pp; English.
 CC The present sequence is that of human oxidoreductase OXR-3, as
 CC deduced from a cDNA clone (see AAA89187) isolated from a lung tumour
 CC cDNA library. The protein shows homology to Escherichia coli
 CC 3-oxoacyl-(acyl)-carrier protein, and includes a short-chain
 CC dehydrogenase signature. OXR-3 is expressed in nervous, reproductive,
 CC cardiovascular and gastrointestinal tissue, and may be involved in
 CC cell proliferation and inflammation. The invention provides OXR-1
 CC to -8 polypeptides (see AAA89926-33) and polynucleotides (see
 CC AAA89185-92). It also provides methods for using these polypeptides
 CC and polynucleotides for diagnosing, treating or preventing disorders
 CC associated with expression of OXR, especially cell proliferative,
 CC neurological, genetic, smooth muscle, and autoimmune/inflammatory
 CC disorders. The proteins can also be used to screen for agonists
 CC and antagonists useful for treating these conditions, while
 CC antibodies that bind to OXR may be used for diagnosis or in assays
 CC to monitor patient treatment.
 XX
 SQ Sequence 237 AA;
 Query Match 23.9%; Score 312; DB 22; Length 237;
 Best Local Similarity 31.6%; Pred. No. 3e-22;
 Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;
 QY 12 VAVTGGASGIGLATARLVGQASAVLLDLPNSGGRAOKKLNCCVFPADVTSEKRV 71
 Db 4 VCAVFGSGRGIGRAVAGLMAKRGRLAVRNTEGAAAGADLGSHLAFSCVAAEHVD 63
 QY 72 QATALAKGKFGRDVAVNCAGI-----AVASKTYNKKQOTHTLEDFQVLDVNLGTF 126
 Db 64 QNTEEEKHKLGRNPLVNAAGINRDLVIRTK-----EDMSQLHTNLLGSM 112
 QY 127 NVIRLVAGMGQNEPDGQGRVLIINTASVAAPFGQQAAYSASKSGITGMPLIARDL 186
 Db 113 LTRCAAMRTMIQ-----QGGSIVNGSIVGLKNSGQSVYSKSGLVGFSALAKEV 166
 QY 187 APGIRVMTIAPGLFTPLTSLPEKYSNFLASQVPPPSRLGDPAEFAHLVQAIIENPFL 246
 Db 167 ARKKIRVAVAPGVPHDMTKDLKE---HLKKNIP-LGRGERTIEVAHNVFLLESPYI 222
 QY 247 NGEVIRLDGAIRM 259
 Db 223 TGHVLYVDGLQL 235
 Db
 RESULT 21
 ID ABB48892 standard; Protein; 247 AA.
 AC ABB48892;
 XX 05-FEB-2002 (first entry)
 DE Listeria monocytogenes protein #1596.
 XX Listeria monocytogenes protein #1596.
 KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KM vitamin B12; bacterial infection; disease.
 OS Listeria monocytogenes.
 XX
 XX WO200177335-A2.
 XX
 XX 18-OCT-2001.
 PD
 XX 11-APR-2001; 2001WO-FR01118.
 PF

XX
 PR 11-APR-2000; 2000FR-0004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangeul L, Couve E, Rusnok C, Fsihi H, Dehoux P;
 PI Dussurget O, Chetoui F, Nedjati H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kretz J, Kuhn M, Ng E, Vazquez-Boland JH,
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Chablit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madueno E, De Pablos B, Wehlund U, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 XX
 DR WPI; 2002-010914/01.
 XX
 PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and
 PT related polypeptides
 PS Claim 6; SEQ ID No 1597; 192pp; French.
 XX
 CC The present invention relates to the genome sequence of Listeria
 CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in L.
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies. Identification of L. monocytogenes and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate L. monocytogenes-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccine compositions for the treatment or prevention of infections by L.
 CC monocytogenes and related organisms.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPD
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 247 AA;
 Query Match 23.5%; Score 306.5; DB 23; Length 247;
 Best Local Similarity 32.0%; Pred. No. 1.1e-21;
 Matches 85; Conservative 45; Mismatches 103; Indels 33; Gaps 7;
 QY 7 SVKGLVAVITGGASGIGLATARLVGQASAVLLDLPNSGGRAQ---KKL---GNNC 58
 Db 2 TLGGKAVAVTGGSGRGIGRIALINLAEGANIFE---NYNGSPEAAEETAKLVAAHGEV 57
 QY 59 VPAPADVTSEKDYOTLALAKGKFGRDVAVNCAGIYASASKTYNKKQOTHTLEDFQVRL 118
 Db 58 EAMKANVAIAEDVDAFFKQAIERFGRVDTLVNNAGITRDNLMRKKE-----DMDDVI 111
 QY 119 DVNLMGTFFVIRLVAGMGQNEPDGQGRVLIINTASVAAPFGQQAAYSASKSGIVGM 178
 Db 112 NINLKGFTLTKRNVSTMMKQ-----RAGKTIINNASVYGLIGNAGQANVYASKAGVIGL 165
 QY 179 TLPIARDLAPIGIRVMTIAPGLFTPLTSLPEKYSNFLASQVPPPSRLGDPAEFAHLVQ 238
 Db 166 TKTTARLAPRGIVNAVAPGFTTMTDKLDEKTEAMIAOLP---LGAAGTTEDIAN 221
 QY 239 AIT-----ENPFGNGEYIRLDGAIRM 259
 Db 222 AVLFLASDASKYITGQTLSDVGGNM 247
 Db
 RESULT 22
 ID AAY95746 standard; Protein; 247 AA.
 XX AAY95746
 AC AAY95746;
 XX

XX 25-OCT-2000 (first entry)
 DT
 XX Bacillus megaterium 3-keto-acyl-CoA reductase Phab.
 DE
 XX Polyhydroxyalkanoate; polyhydroxybutyrate; transgenic plant; Phab;
 KW 3-keto-acyl-CoA reductase.
 XX
 OS Bacillus megaterium.
 XX
 PN WO200040730-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 07-JAN-2000; 2000WO-US00364.
 XX
 PR 07-JAN-1999; 99US-0115592.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 XX
 PI Cannon MC, Cannon FC, Mccool GJ, Valentin HE, Gruys KJ;
 XX
 DR WPI: 2000-532624/48.
 XX
 DR N-PSDB: AAA50142.
 XX
 PT New nucleic acid fragment encoding proteins involved in
 PT polyhydroxyalkanoate (PHA) biosynthesis, useful in the production of
 PT transgenic plants or recombinant plant cells which can express PHAs
 PT such as polyhydroxybutyrate -
 PS
 PS Claim 85; Page 137-138; 153pp; English.
 XX
 XX The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase
 CC protein of Bacillus megaterium. The sequence was deduced from an
 CC open reading frame identified in an isolated 7,916 bp fragment of
 CC B. megaterium strain 11561 genomic DNA (see AAA50142). The 7,916 bp
 CC DNA fragment includes genes encoding proteins (see AA95743-47)
 CC involved in polyhydroxyalkanoate (PHA) biosynthesis. Nucleic acids
 CC encoding these proteins are useful for creating transgenic plants or
 CC recombinant host cells which have the capability of expressing PHAs
 CC such as polyhydroxybutyrate, polyhydroxyvalerate,
 CC polyhydroxyhexanoate, polyhydroxyoctanoate, polyhydroxydecanoate or
 CC their copolymers. Claimed methods for preparing a PHA involve
 CC obtaining a plant or a cell comprising a nucleic acid sequence
 CC a 3-keto-acyl-CoA reductase (especially the present sequence), and
 CC a nucleic acid encoding a PHA synthase (see AA95747), and growing
 CC the plant or cell under conditions suitable for PHA production.
 CC
 XX
 SQ Sequence 247 AA:
 Query Match 23.2%; Score 303; DB 21; Length 247;
 Best Local Similarity 29.1%; Pred. No. 2.4e-21;
 Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;
 QY 7 SVKGIATVITGGASGIGLTAERLVGQ-----ASAVLLDIPNSGGEGQAK 53
 DB 3 TLGGKVAIVTGGSKGGAALITRELASNGKVAVANNSSKESDAIYKEIKDNGER---- 58
 QY 54 LGNNCVFAPADVTSEKDVOTALALAKGFRVDVAVNACGIAVASKTYNLRK-GQTHLE 112
 DB 59 -----IAVQADVSYYQAKHLEETRAKAGQDLIVNNAIGI---TRDRSFKKIGE----E 106
 QY 113 DFRQVLDVNLMTGFNIRLVAGMGONEDDGGQKRVITNTSVAFSEQVQAAVSAK 172
 DB 107 DMKKVIDVNLHSHYNTTSALTHLESE---GGR---VINISITIQAGGFGQNTSAK 160
 QY 173 GGIVGMLPIARDLIGIRVMTIARLFGTPLLTLSPKVSNFLASQVFPFSGDPAE 232
 DB 161 AGHLGTTKSLALELATGTVYVNAICGFIETEMVMAIPEDVRAKIVAKIP-TRRLGHAE 219
 QY 233 YAH-LVQATLENFPLNGEVIYRLDGAIRM 259
 DB 220 IARGVYLLAKDGAIVITIGQDLININGLYM 247

RESULT 23
 AAU28296
 ID AAU28296 standard; Protein: 288 AA.
 XX
 AC AAU28296;
 XX
 DT 18-DEC-2001 (first entry)
 DE
 DE Novel human secretory protein, Seq ID No 653.
 XX
 KW Human: secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HXSEQ INC.
 XX
 PI Tang YF, Liu C, Aundri V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QH, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 DR WPI: 2001-589934/66.
 XX
 DR N-PSDB: AAS45196.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 PS
 PS Example 2; SEQ ID No 653; 107pp; English.
 XX
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I) (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and

Page 16

SQ Sequence 288 AA;

0Y 1 MAACRSVKGLVAVITGGASGLATAERLVGGASAVLLDLLPNSGGEAQAKKLGNNCVF 60

QY 61 APADVTSEKDVTALALAKGKEGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFORVIDV 120

121 NLMGTENVIRLVAGEMGONEPDOGGORGVITNTASVAAFEFGOVGOAAYSASKGTVGMTT. 180

00 181 BTABDI ABICIBINMETABCI ECTBTITMET DEVENETI ACORDED - 004

[illegible]

ABPS900 / Standard; Protein; 205 AA.
XX

DT 24-JUL-2002 (first entry)
XX

Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX

FD
XX
30-APR-2002.

PR 14-AUG-1997; 97US-055779P.
PR 08-NOV-1997: 97US-06496AP

XX
XX

DR N-PSDB; ABN92212.

XX, polyepoxide, useful for diagnosing and treating bacterial infections.

CC ABN90538 to ABN93374 represent *Staphylococcus epidermidis* open reading

can also be used in the diagnosis and treatment of bacterial infections

CC cycle or inhibit S. epidermidis infection.
CC N.B. The sequence data for this patent did not form part of the printed

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPRO web site.

Sequence	263	AA
...		
5Q		

QY 12 VAVITGGASGLTAERLVGGASAVLLDLPNSGGEAQAKK---GNNCVFAPADVTSE 68

OV 69 KDVOTATA LAKGKFG RVDVAVNCAGI AVASKTYNLKKGOTHTLED FORVL DVNLMTFNV 1

00 139 TPIVACEMCONEPDOGGOCVITNTASVAAEEGCVGOAAVSSBSKGGTVMETIPIABDIAP 1

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Db 236 NVVSFLAGSDSDYITGQTIIVDGM 261

RESUL 2
AAR89323

AAK89323;
AC
XX

DE Rape leaf beta-ketoacyl-ACP-ketoreductase.

KW plastid; stroma; transit peptide; cassette; antisense; oilseed;

Brassica napus.

peptide
1.55
/note= "Transit peptide"

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PI Chase D, Elborough K, Fentem PA, Slabas AR, White A;
 XX WPI; 1996-105914/11.
 DR N-PSDB; AAQ99305.
 XX

PT New isolated rape beta-ketoreductase DNA - used to develop plants
 XX with lower or higher oil contents or with altered oil compsn.
 XX

PS Claim 2; Page 16; 29pp; English.

CC The sequence corresponds to a rape leaf beta-ketoreductase encoded
 CC by a cDNA insert in plasmid pJRL6.2 in Escherichia coli XL1-Blue.
 CC A plastid stroma targeting transit peptide is present. DNA
 CC encoding the protein may be inserted in a vector or expression
 CC cassette in sense or antisense orientation for expression in an
 CC oilseed plant, e.g. for production of transgenic rape plants with
 CC low or modified oil content, diversion or metabolism to alternative
 CC storage compounds, e.g. starch, protein or engineered polymers, or
 CC production of plants with enhanced oil content. The DNA may also
 CC be used as a probe to obtain similar genes from other plants. The
 CC transit peptide may be used to direct other proteins to leaf
 CC plastids.
 CC

XX Sequence 315 AA;
 SQ

Query Match 22.6%; Score 295; DB 17; Length 315;
 Best Local Similarity 30.5%; Pred. No. 2e-20;

Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6;

QY 4 ACBSYKGLVAVITGGAGSLGLATRAERLYVGASAVLLDLPNSGGEA-----QAKKLGNC 58
 DB 66 AVKVESPVVVVVGASRGIGKAIKLSL-GRAGCKVLVNVARSASKEEVSQTEAYGGQA 124
 QY 59 VFAPADVTSEKDYOTALALAKGFRGVDAVNCAGIYASKTYNLKKGQTHLEDFQRYL 118
 DB 125 ITFGDVSKEDVEMMKTAIDAMGTIDVVVNNAGITRDILLRMKKSQ-----WDEVI 178
 QY 119 DVNLMTFNVYRLVAGKQNEPDQGRGVYINTASVAAFEGOVGOAAYSASKGIYGM 178
 DB 179 DLNLTVFLCTQAATKIMRK-----RKGRINIISVGLIGNIGQANYAARAGYIGF 232
 QY 179 TLPIARDLAPIGIRVMTIAPGLFCTPLPLTSIPEKVSNFLASOVFPSPRLGDPAYAYLVQ 238
 DB 233 SKTARREGASRNINNVVCPFIASDMYATKLGEMEKKIIGITPL-GRYGPEDVAGIVE 291
 QY 239 AILENP---FLNGEVIRIDGAI 257
 DB 292 FLALSPASVITGQAFYIDGSI 313

Search completed: June 23, 2003, 14:28:35
 Job time : 41.6667 secs

RESULT 10
 F83098
 Probable short-chain dehydrogenase PA4389 [imported] - *Pseudomonas aeruginosa* (strain PA
 C:Species: *Pseudomonas aeruginosa*
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83098
 C:Stover, C.K.; Plam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Litt
 e, Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10584043
 A:Accession: F83098
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-252 <STC>
 A:Cross-references: GB:AE004854; GB:AE004091; NID:9950606; PIDN:AG07777.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4389
 A:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match	27.2%	Score 355;	DB 2:	Length 252;
Best Local Similarity	35.1%	Pred. No.2.9e-20;		
Matches	94;	Conservative 40;	Mismatches 100;	Indels 34; Gaps 7;
QY	8	VKGLAVYTTGASGSGIGLATAERLVGOGASAVLLLPN-----	SSGEAQAARKIG	55
DB	3	LKDKIITITGCGCGGGRAMGEYLAGKGRALATVLDREDEAVAACKAAAGDARA----		58
QY	56	NNCVFAPADVYSEKMDYQATALAGKGFPRVAVVANCAGINAVSKTYNKKSGQTH--TLED	113	
DB	59	-----YVCNVADDEEYTHMVAQVASFDAIINGLVNNAIGLIDDLGITIKKKDQLSKMSLQAQ	113	
QY	114	FORVLVDNLMTGFENVYIRLVAGEMKQ--NEPDQGGORGYVINTASYAAFEVGGQAAYSAS	171	
DB	114	MOSYVDVNLMTGFTLCRTREVAARKMIETKNE-----GAIVNISSISR--AGNMGAQANSAA	165	
QY	172	KGGIVGMLTLPATRDAPIGIRVMTIAPLPFGPILTTSPEKYANVLASQVFPFSPRLGPA	231	
DB	166	KAGVAADLVVMAKELARAGIRVAGVAGAPFIETEMTAKGPKPELLEKMTAGITFL--RMGKRV	224	
QY	232	EYALHLYOAIITENPFLNGEYIRLDGARIM	259	
DB	225	ETASHVAYITFENDYTGIVLELDGGRL	252	

RESULT 11
 P97338
 3-ketocacyl-acyl carrier protein reductase [Imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: P97338
 R:Noilling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359335
 A:Accession: P97338
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1249 <KUP>
 A:Cross-References: GR:AE001437; PIDN:NAK81497.1; PID:415026670; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC3574
 C:Superfamily: ribitol dehydrogenase: short-chain alcohol dehydrogenase homology

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QY      8 KKGIVATITGASGLGATLAEITLYGOGASAVLTDLPSPGGGAO-----AKKIGNNCYAP 62
Db      5 LSGVAAVATGGRGRLGRIALKLAEAGANLV-VNRSSEAEYQKLMEITELSGKAAVAK 63
QY      63 ADVTSEKDVOOTALANGKFGGRVDVAVNCAGIAVASTYKLGKQHTLEDPOFVLDVNL 122
Db      64 ADISKYDEAEETIKKALDEYGTVDILVNNAGITDNLILRKE-----EDFQSVIRVNL 117
QY      123 MGTENVIRLVAEGEKGNPPDGGGORYILINASVAAEEGQVGOAAVSASRGYIGMTLPI 182
Db      118 KGAEFCIKHISRVMKK-----KSGKITINSSVIGLIGNAGQVNVAAAKGIGIMKRSV 171
QY      183 ARDLAPIGIRVMTAPLFGTPLLTSLEPKYANFLASQVPPSPRLGDPAEYAHVQAIIIE 242
Db      172 AKELASRGITVNAVAAGIKISDMTDALTDKQRESIYAAVPL-NKVGAEAEVANLVFLAS 230
QY      243 --NPELNGEVRRLGCAIRM 259
Db      231 DLSSTIITGOVINVDGQVMV 249

```

RESULT 12
 H72219
 3-oxoacyl-(acyl carrier protein) reductase - *Thermotoga maritima* (strain MSB8)
 C:Species: *Thermotoga maritima*
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: H72219
 R:Neelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.T.; Haft, D.H.; Hildreth, G.E.;
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; PMID:99287316; PMID:10360571
 A:Accession: H72219
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1246 <ARN>
 A:Cross-references: GB:AE001811; GB:AE000512; NID:g4982291; PIDN:AAJ36790.1; PID:g4982291
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1724
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F:6-185/Domain: short-chain alcohol dehydrogenase homology <SMD>
 Query Match 26.3%; Score 343; DB 2; Length 246;
 Best Local Similarity 33.7%; Pred. No. 2,4e-19;
 Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;

[illegible]

Query Match	26.5%;	Score 345.5;	DB 2;	Length 249;
Best Local Similarity	33.2%;	Pred. No. 1.6e-19;		

RESULT 13
C83961

C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
C:Accession: C63961
R:Name: H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 26, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C63961
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1246 <SNO>
A:Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BA06210.1; GSPDB:GN00
C:Genetics:
C:Gene: fabG
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.7%; Score 335.5; DB 2; Length 246;
Best Local Similarity 34.2%; Pred. No. 9,2e-19;
Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

QY 8 VKGLAVITGASGSLGATAERLVGGASAVLLDPLNSGE-----AQAKLGNVCV 59
DB 2 LQKKAIVTGSRSRGIGRATAMELARHGANNVY---NAGKREKAEKVAAIKELGEVAI 57
QY 60 FAPADVSEKOVQALALAKGKRGVDVAVNCAGIAVASKTYNKKGGTHLEDFORYLD 119
DB 58 AIGQADVDSSEVQAMVKETIDTFGANVLDLVNNAAGTRNLNRKKE-----EDMDAVID 111
QY 120 VNLGTFNVIRLVAGSEWQNEPDGGQR-GVIINTASYAALEGQVGAAYSAKSGGIYGM 178
DB 112 TNLKVFHCSKAVTRPMK-----QRFGRINNSVVGAIAGNAGQANYAAKAGVIGL 164
QY 179 TLPIRDLAPIGIRMTAPGTFGPTLTSPEKVAANFLASQVPPPSRLGPAEYAHLYQ 238
DB 165 TKTLARELANNTIYNAAPGFIETDMGELPEDEVKAKMLQIPL-ALNGPSEYAKAVR 223
QY 239 AIEN-PFLNGEVTRLDCAIRM 259
DB 224 FLASDASYLTGGITIHVNGMYM 246

RESULT 14
31084
3-oxoacyl-[acyl-carrier-protein]-reductase (car-1) [imported] - Neurospora crassa
N:Alternate names: protein B2A19.180
C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-May-2001
C:Accession: T51084
R:Schulte, U.; Aign, V.; Hohsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, July 2000
A:Reference number: 225286
A:Accession: T51084
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-297 <SCH>
A:Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.180
A:Experimental source: BAC clone B2A19; strain OR74A
C:Genetics:
A:Gene: NCSP:B2A19.180
A:Map position: 6
A:Insertions: 218/1; 249/1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.7%; Score 335.5; DB 2; Length 297;
Best Local Similarity 31.7%; Pred. No. 1.2e-18;
Matches 97; Conservative 39; Mismatches 103; Indels 67; Gaps 8;

QY 6 RSVKGLAVITGASGSLGATAERLVGGASAVLLDPLNS-----GGEQ 50
DB 2 RSLNKAQVITGGGSGIGAIARRLYBECSTVTLGRTSTLORASQSLISQPLHSPQ 61
QY 51 AKKLGNNCFAPADVSEKOVQAL-ALAKGKRGVDVAVNCAGIAVASKTYNKKGG 106

Db	62	QPSPTKRVSYHPLNLTSSASWEDILQSNSSGKGRVDILLINCAGITORSPLMKT	115
Qy	107	QTHLLEDFQRILVYNLMGTNNVIRLVAGEGONEP-----DOGG-----	145
Db	116	---STEEEGLLDNLNGVYLGCCKFVRAMLRNPSQOHRVKADBSGACVHEGTREEG	172
Qy	146	-----ORGVINTASVAAFEGOVGOAAYSASKSGIVGCTLPDIARDLAFGI	191
Db	173	KGEKGGGVREGVQERGVILNVASLLAOKGVIGTSYVAANKAGVAGLITSLAHEYGRGI	232
Qy	192	RYMTIAGLFEETPLLTSLPERKANFLASOVFPFRLLDPDAEVAAHLVQAIIENPLNGEVI	251
Db	233	RVNAVLPGIYITDWTGLKNP---SILOQIPL-GRFQTTDEVDALPFLIKNPANNCVL	288
Qy	252	RLDGAII	257
Db	289	NLDGGL	294

RESULT 15

S22450
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor. NADPH-dependent
N.Alternate names: beta-ketoacyl-ACP reductase
C.Species: Cuphea lanceolata
C.Date: 16-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 17-Mar-2000
C.Accession: S22450; S19832
R.Klein, B.; Pawlowski, K.; Hoejck-Grandpierre, C.; Schell, J.; Toepfer, R.
Mol. Gen. Genet. 233, 122-128, 1992
A.Title: Isolation and characterization of a cDNA from Cuphea lanceolata encoding a b
A.Reference number: S22450; MUID:92293104; PMID:1376402
A.Accession: S22450
A.Molecule type: mRNA
A.Residues: 1-320 <KLE>
A.Cross-references: EMBL:X64566; NID:g18045; PID:CAA45866.1; PID:g18046
A.Experimental source: Immature embryo
C.Genetics:
A.Gene: CLK+27
A.Genome: nuclear
C.Function:
A.Description: EC 1.1.1.100 [validated, MUID:92293104]
A.Pathway: fatty acid biosynthesis
A.Note: Integral part of the fatty acid synthase type II
C.Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C.Keywords: chloroplast; fatty acid biosynthesis; NADP: oxidoreductase
F.1-63/Domain: transit peptide (chloroplast) #status predicted <RNP>
F.64-320/Product: 3-oxoacyl-[acyl-carrier-protein] reductase #status predicted <NAT>
F.78-358/Domain: short-chain alcohol dehydrogenase homology <SADP>
F.227/Active site: Tyr #status predicted

Query Match 25.7%; Score 335; DB 2; Length 320;
Best Local Similarity 32.7%; Pred. No. 1,4e-18;
Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;

Qy	2	AAAGSVAGLVAVITGGASGLGATAEKRVGGAVALLDLPNSGGA-----QAKKIGN	56
Db	69	AAAGGSVESPVAVITGASRGVIGKATALLD-GAAGCKVAVNARSSKEAEVSKLEAFRG	127
Qy	57	NCVFAPADVTSEKDDVOTALAKGKFRGVADVAVNACGIAVASKYTNLKKGQTHLEDFOR	116
Db	128	QALTEGDFGVDSKEDVEAMIKTAVDAMGVTDILVNNAGTIRPGLLMKMKSQ-----WQE	181
Qy	117	VDVNLKGFENVIRLVAGEGONEDDGGQREVIINTTASVAFBEQOVGOAAASASKGIY	176
Db	182	VIDLNTGVFELCTQAAAKTKMKR-----KKRRIINIASVGLVNNAGANTSAKAGVI	235
Qy	177	GNTLPDIARDLAFIGIRVMTIAPGLEGTPLLTSLPERKANFLASOVFPFRLLDPDAEVAAHL	236
Db	236	GFTKTVAREYASRNINNVANVAPGFTSSDMTSLRGDINKKILETIFPL-GRYGQPEEVAGL	294
Qy	237	VQAIIENP---FLNGEVIRLDGAIRM	259
Db	295	VEFLAINPSSSYTGVQVFTIDGKMTM	320

RESULT 16

3-oxoacyl-[acyl-carrier protein] reductase [imported] - Nostoc sp. (strain PCC 7120)
AH2042
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AH2042
R:Kakeko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, K.; Nakaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DN: Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2042
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAW73593.1; PID:G17130984; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: fabG
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.7%; Score 334.5; DB 2; Length 251;
Best Local Similarity 33.1%; Pred. No. 1,1e-18;
Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

QY 1 MAACASVGVAVITGGASGLATAEELVGGASAVL-----VLLDPNNGG 47
DB 1 MALSLNMGQVAVITGGASRGIGRALELAETAYVAVNNASSSTADAEVVAETGGAG 60
QY 48 EAQAKKIGNVCVAPADVTSEKDVOTATALAKGFRVDVAVNCAGIYASKTYNKKQ 107
DB 61 EAVALK-----ADVQVQVNLINGAIDKFKRIDILVNNAGITRDLILMKRP-- 109
QY 108 THLEDFORVDVNLGTFNVAIRVAGEGONPEPQGGRGVITNTASVAAFEQVGAA 167
DB 110 ----EDMQAVIDNLNLGFLCTRAVSKMLKO-----RSGRIITITSVAGCMGPGQAN 159
QY 168 YSASKGIVGKMTLPARDLAPIGIRVMTAPGLFTPLTSLPEKVANFLASQVPPSR 227
DB 160 YSAAKGVIGFTKVAKEKELASRGITVYNAVAPGFIATDMTSMK---SEGIQYIPL-GRY 215
QY 228 GDPAEVAHLVQALIEP---FLNGEYIRLDGAIRM 259
DB 216 GQPEELAGVRFPLADPAAAYITGOVFNVDGGMV 250

RESULT 17

3-oxoacyl-[acyl-carrier protein] reductase BH3896 [imported] - Bacillus halodurans (strain
H84136
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84136
R:Nakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: H84136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <STO>
A:Cross-references: GB:AP001520; GB:BA000004; NID:G10176401; PIDN:BAW07615.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3896
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.5%; Score 332; DB 2; Length 246;
Best Local Similarity 34.2%; Pred. No. 1.7e-18;
Matches 91; Conservative 40; Mismatches 95; Indels 40; Gaps 8;

QY 8 VKGLVAVITGGASGLATAEELVGGASAVL-----LPNSGGEAOKKLG 55
DB 3 LNCVAMITGGAGGIAATATKARFAGAKVYICDVVEEVAKTVAEIQGGGA-----LG 58
QY 56 NNCVFPADVTSEKDVOTATALAKGFRVDVAVNCAGIYASKTYNKKQTHLEDFQ 115
DB 59 ----SWVDYQKDVKNVINYIEERFELDVVYNNAGITADAQTNMTDAQ-----WD 107
QY 116 RVLDVNLGTFNVAIRVAGEGONPEPQGGRGVITNTASVAAFEQVGAAVSAKSGI 175
DB 108 DVIDVNLKGFYITQEVTTIMKQ-----KRGVILNASSVSGYGNFGQTNNAASKGCV 161
QY 176 VGMTLPARDLAPIGIRVMTAPGLFTPLTSLPEKVANFLASQVPPSRIGDPAE--- 232
DB 162 NGMTKTAKELGIRVAVNNAVAPGFIPTETKPKPKVAKVMEKAVL-NRLGTVEVAN 220
QY 233 -VAHLVQALIEPFLNGEYIRLDGAI 257
DB 221 GFAFL-ASDEASTITETIADIGV 244

RESULT 18

3-oxoacyl-[acyl-carrier protein] reductase VC2021 [imported] - Vibrio cholerae (strain
F82128
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82128
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.
charison, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Drysdale, I.; Sellers
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:2040683; PMID:10952301
A:Accession: F82128
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <HEI>
A:Cross-references: GB:AE004276; GB:AE003852; NID:9656555; PIDN:AAF95169.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2021
A:Map position: 1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.3%; Score 330.5; DB 2; Length 248;
Best Local Similarity 32.0%; Pred. No. 2.3e-18;
Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;

QY 7 SVKGLVAVITGGASGLATAEELVGGASAVLIDLPNSGGEAOKKIGNVCVAPADVT 66
DB 6 NLEGVAVITGGASRGIGRALELAETAYVAVNNASSSTADAEVVAETGGAG 65
QY 67 SEKVQVOTATALAKGFRVDVAVNCAGIYASKTYNKKQTHLEDFORVDVNLGTF 126
DB 66 NPESTEAVLKAITDFEGVDLVNNAAGITRDLILMKRKE-----EKSJMEINLSIF 119
QY 127 NVIRLVAGEGONPEPQGGRGVITNTASVAAFEQVGAAVSAKSGIVGKMTLPARD 186
DB 120 RLKSAVILGMMKK-----RGRILNVSVVGTMGNAGYAAAKAGVIGFTKSMAREV 173
QY 187 APGIRVMTAPGLFTPLTSLPEKVANFLASQVPPSRIGDPAEVAHLVQALIEP--- 244
DB 174 ASRGVAVTAPGFIETDMTALNDDEORTATLAQV-AGRLGDPRELSAV-AFLASPEA 231
QY 245 -FLNGEYIRLDGAIRM 259
DB 232 AVITGETLHVNGGMV 247

RESULT 19

3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) [imported] - Streptococcus
E37919
C:Species: Streptococcus pneumoniae

Query Match	25.2%;	Score 328.5;	DB 2;	Length 243;
Best Local Similarity	35.1%;	Pred No. 3.2e-18;		
Matches 88;	Conservative 36;	Mismatches 104;	Indels 23;	Gaps 6;

RESULT 20

Query Match	25.2%;	Score 328.5;	DB 2;	Length 260;
Best Local Similarity	37.3%;	Pred. No. 3.4e-18;		
Matches 97;	Conservative 33;	Mismatches 109;	Indels 21;	Gaps 9

[illegible]

RESULT 21

Query Match	25.18;	Score 327.5;	DB 2;	Length 243;
Best Local Similarity	34.78;	Pred. NO. 3.8e-18;		
Matches 87; Conservative	37;	Mismatches 104;	Indels 23;	Gaps 6;

RESULT 22

A;Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: F86721
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-243 <STO>
A:Cross-references: GB:AE005176; PID:q12723693; PIDN:AAK04872.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: fabG1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.0%; Score 326.5; DB 2; Length 243;
Best Local Similarity 31.7%; Pred. No. 4.5e-18;
Matches 82; Conservative 48; Mismatches 104; Indels 25; Gaps 6;

QY 8 VAGLVAVITGASGLTAERLVGASAVLLDIPNSGSAOKAKL-----GNNCVF 60
DB 3 INKNVAVITGSTRIGKALDQFAKASRLII-----NGRSISELLAEFTAGYKAVG 57
QY 61 APADYSEKDYOTALAKGKFRVAVNCAGIYASRTYLNKKQTHLEDFORVLDV 120
DB 58 ISGDISKSEDAKQWAEALLETLSVDILVNNAGI--TRDGLSLKKSE---EDFESVLKI 111
QY 121 NLMGFNRYRLVAGENGQNEPDQGGQGVYIINTASVAAPFEGOVGAASASAGGIYVMTL 180
DB 112 NLTGAFNMTQAVL-----KPMTRARSGAILINISSVGLMGNAQANTAAASKAGLIGLTR 165
QY 181 PIARDLAPIGIVMTIAPGLFGPPLTSLPEKVNFLASQVFPFRLGDPAEYAHVQAI 240
DB 166 SIREVYAAKRVNNAVNAAPFIESDMTEVLSDYKNAKMGQIM-KRFGMEELIATATQFL 224
QY 241 IENPFLNGEYIRLDGAIYM 259
DB 225 AEQEVMTQGVLTIDGGVSM 243

RESULT 23
D90481
hypothetical protein fabG-9 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: D90481
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Koser, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.
Submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: D90481
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-299 <KUR>
A:Cross-references: GB:AE006641; NID:q13816394; PIDN:AAK43107.1; GSPDB:GN00155
C:Genetics:
A:Gene: fabG-9
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.3%; Score 317; DB 2; Length 299;
Best Local Similarity 32.5%; Pred. No. 3.2e-17;
Matches 83; Conservative 47; Mismatches 107; Indels 18; Gaps 5;

QY 12 VAVITGASGLTAEERLVGASAVLLDIPNSG---EAQAKKLGNNCVFAPAYTSE 68
DB 4 VSITTGAKGIGAGIATGRLKOGYAVVADYDEAGYRNNHRCGDISFFTKTIVSSB 63
QY 69 KDYOTALAKGKFRVAVNCAGIYASRTYLNKKQTHLEDFORVLDVNLMTGFNY 128
DB 64 MDVSNMVEKYGKRGIDVYVNNAGIFSGKSI-----EQGITDERMRYETMLTGVMIC 118
QY 129 IRLVAGENGQNEPDQGGQGVYIINTASVAAPFEGOVGAASASAGGIYVMTLPIANDLAP 188
DB 119 SKYAVKTKNN-----GGVIVINASTRAFOSEPNEPEYASAKGIIATLHSLAVLSK 171

DB 172 YNIRVYISPGWLDTSRMQVPPRESTLSGLDHQHTLRVRKPEDVASIVTFVSDASW 231
QY 246 LNGEVITLDGAIYMQ 260
DB 232 ISGVNFTIDGMATVK 246

RESULT 24
H98137
3-oxoacyl-(acyl-carrier protein) reductase (3-ketoacyl-acyl carrier protein reductase
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: H98137
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Gurolo, B.; Goldm
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: H98137
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-259 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK88626.1; PID:q15158345; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L126
A:Map position: linear chromosome
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.3%; Score 316.5; DB 2; Length 259;
Best Local Similarity 36.2%; Pred. No. 2.9e-17;
Matches 94; Conservative 44; Mismatches 91; Indels 31; Gaps 10;

QY 9 KGLVAVITGASGLTAERLVGASAVLLDIPNSGGEAOKAKLNN-----CYFAP 62
DB 9 KGAVA-ITGASGSGIFSTQILMARQMPWLLDKREALDIACEKIDIMRGIVC--- 63
QY 63 ADVTSKDYOTALA-LAKGKFRVAVNCAGIYASRTYLNKKQTHLEDFORV 118
DB 64 -DVADASIEMAFALPANGDHAVDVAVVNSAGICID-----KLSVDSVEFRRIY 116
QY 119 DVNLMGTNRYRLVAGENGQNEPDQGGQGVYIINTASVAAPFEGOVGAASASAGGIYVMTL 178
DB 117 DVNLTGSPAVAAARWLESD-----VAGSIVINISSVSGMGRGSAVYASAGVNL 171
QY 179 TLPARDLAPIGIVMTIAPGLFGPPLTSL-PEKVNFLASQVFPFRLGDPAEYAHV 237
DB 172 TMMVAMNELGSGIRVNAIAPGPVDTPLTQAVHTENVRDQMSRPV-HRYGRTEIASAV 230
QY 238 QAIEN--PFLNGEYIRLDG 255
DB 231 AFLVSDASVINGVLAVDG 250

RESULT 25
A13149
3-oxoacyl-(acyl-carrier protein) reductase [imported] - Agrobacterium tumefaciens (st
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: A13149
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Moks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo-
erage, G.; Gillet, W.; Grant, C.; Gnehm, D.; Kutyavin, T.; Levy, R.; Li, M.; McCa-
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreespan, W.; Perry, M.; Gordon-Kam-
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: A13149
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-259 <KUR>
A:Cross-references: GB:AE008689; PIDN:AA145615.1; PID:q17743336; GSPDB:GN00187

Thu Jun 26 06:55:04 2003

us-09-931-186-20.rapb

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.333 Seconds
(without alignments)
1388.950 Million cell updates/sec

Title: US-09-931-186-20
Perfect score: 1304
Sequence: 1 MAACRSYKGLVAVITGAS.....ENPLNGEVRIDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 segs, 108206813 residues 417779

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304	100.0	261	10	US-09-931-186-20
2	1301	99.8	261	10	US-09-931-186-23
3	1300	99.7	261	10	US-09-931-186-8
4	1299	99.6	261	10	US-09-931-186-2
5	1290	98.9	261	10	US-09-931-186-4
6	1290	98.9	261	10	US-09-931-186-6
7	1137	87.2	227	9	US-09-984-245-245
8	1137	87.2	227	9	US-09-966-262-245
9	1137	87.2	227	9	US-09-983-966-245
10	1137	87.2	227	9	US-09-983-966-245
11	666.5	51.1	388	9	US-09-920-923-41
12	333.5	25.6	259	10	US-09-931-186-17
13	328.5	25.2	243	10	US-09-815-242-1360
14	328.5	25.2	243	10	US-09-815-242-13581
15	320.5	24.6	245	10	US-09-815-242-10921
16	314	24.1	237	9	US-10-175-696-14
17	314	24.1	237	10	US-09-823-901-2
18	308.5	23.7	253	10	US-09-931-186-15
19	303	23.2	247	9	US-09-479-040-9
20	297.5	22.8	267	9	US-09-773-748-1
21	296.5	22.7	262	9	US-10-307-385-6
22	296.5	22.7	262	10	US-09-802-853-6
23	293.5	22.5	270	9	US-09-978-295A-468
24	293.5	22.5	270	9	US-09-978-697-468
25	293.5	22.5	270	9	US-09-978-192A-468
26	293.5	22.5	270	9	US-09-999-832A-468
27	293.5	22.5	270	9	US-09-978-189-468
28	293.5	22.5	270	9	US-09-978-608A-468
29	293.5	22.5	270	9	US-09-978-608A-468
30	293.5	22.5	270	9	US-08-978-403A-468
31	293.5	22.5	270	9	US-09-978-644A-468
32	293.5	22.5	270	9	US-09-978-585A-468
33	293.5	22.5	270	9	US-10-017-081A-468
34	293.5	22.5	270	9	US-09-978-824-468
35	293.5	22.5	270	9	US-09-981-915A-468
36	293.5	22.5	270	9	US-09-999-833A-468
37	293.5	22.5	270	9	US-10-167-749-468
38	293.5	22.5	270	9	US-09-968-585A-468
39	293.5	22.5	270	9	US-09-978-423A-468
40	293.5	22.5	270	9	US-10-013-921A-468
41	293.5	22.5	270	9	US-09-978-193A-468
42	293.5	22.5	270	9	US-10-013-929A-468
43	293.5	22.5	270	9	US-10-016-177A-468
44	293.5	22.5	270	9	US-09-999-830A-468
45	293.5	22.5	270	9	US-09-978-757A-468
46	293.5	22.5	270	9	US-09-978-167B-468
47	293.5	22.5	270	9	US-09-978-643A-468
48	293.5	22.5	270	9	US-10-166-709A-468
49	291.5	22.4	244	10	US-09-815-242-10126
50	288	22.1	263	10	US-09-815-242-14092
51	287.5	22.0	244	9	US-09-849-092-13
52	287.5	22.0	246	9	US-09-364-847-6
53	287.5	22.0	641	9	US-09-364-847-10
54	287.5	22.0	641	9	US-09-364-847-19
55	287.5	22.0	642	9	US-09-364-847-59
56	287.5	22.0	642	9	US-09-364-847-61
57	287.5	21.7	203	9	US-10-175-696-19
58	283.5	21.7	203	10	US-09-823-901-7
59	278	21.3	258	9	US-09-738-626-6436
60	276.5	21.2	286	10	US-09-815-242-11860
61	276	21.2	285	10	US-09-815-242-10241
62	274.5	21.1	254	9	US-09-978-758-2
63	274.5	21.1	272	10	US-09-815-242-12668
64	274	21.0	206	9	US-09-997-816-4
65	273.5	21.0	251	10	US-09-815-242-5689
66	271.5	20.8	246	10	US-09-815-242-5461
67	271.5	20.8	246	10	US-09-815-242-12123
68	271.5	20.8	246	10	US-09-815-242-12803
69	271.5	20.8	246	10	US-09-815-242-13100
70	268.5	20.6	242	10	US-09-815-242-10974
71	268	20.6	251	9	US-10-272-419-20
72	267	20.5	256	10	US-09-954-314-14
73	267	20.5	276	9	US-09-944-160-24
74	266.5	20.4	258	9	US-10-156-055A-1
75	264.5	20.3	252	9	US-09-910-033A-2
76	263	20.2	253	10	US-09-815-242-11842
77	261	20.0	261	9	US-09-971-556-74
78	258	19.8	261	10	US-09-940-037A-29
79	253.5	19.4	266	9	US-09-981-353-40
80	253.5	19.4	266	9	US-09-885-303A-22
81	253.5	19.4	266	9	US-10-205-823-176
82	253.5	19.4	266	10	US-09-931-186-18
83	249	19.1	221	10	US-08-764-853-553
84	246.5	18.9	261	10	US-09-815-242-10846
85	246.5	18.9	262	10	US-09-815-242-10597
86	242	18.6	255	10	US-09-931-186-14
87	241	18.5	251	10	US-09-922-001-16
88	240	18.4	247	10	US-09-815-242-11893
89	240	18.4	258	10	US-09-954-314-12
90	239.5	18.4	274	9	US-09-976-059-17
91	236	18.1	271	9	US-09-815-242-13397
92	236	18.1	272	10	US-09-815-242-13679

93 235 18.0 311 9 US-09-738-626-3819 Sequence 3819, Ap
94 231 17.7 261 10 US-09-815-242-5613 Sequence 5813, Ap
95 227.5 17.4 247 10 US-09-815-242-11342 Sequence 11342, A
96 227 17.4 254 10 US-09-741-668-411 Sequence 411, App
97 224.5 17.2 247 10 US-09-815-242-11514 Sequence 11514, A
98 222.5 17.1 900 9 US-10-060-230-15 Sequence 15, App1
99 222.5 17.1 900 9 US-10-060-230-17 Sequence 17, App1
100 218.5 16.8 253 10 US-09-815-242-10279 Sequence 10279, A

ALIGNMENTS

RESULT 1
US-09-931-186-20 Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGRE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 261
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214A
US-09-931-186-20

Query Match 100.0%; Score 1304; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e-109;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGGAOKLGNVCYF 60
DB 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGGAOKLGNVCYF 60
QY 61 APADVTSEKDVOTATLAKKGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFOVRLDV 120
DB 61 APADVTSEKDVOTATLAKKGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFOVRLDV 120
QY 121 NMGTENVIRLVAGEMGQNEPDGQGRVYIINTASVAAFEGOVGAAYASAKGIVGNTL 180
DB 121 NMGTENVIRLVAGEMGQNEPDGQGRVYIINTASVAAFEGOVGAAYASAKGIVGNTL 180
QY 181 PIARDLAPIGIRVMTIAGLFTPLLTSLPEKXANFLASOVPPSRIGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAGLFTPLLTSLPEKXANFLASOVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

US-09-931-186-23
Sequence 23, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGRE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 261
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214S
US-09-931-186-23

Query Match 99.8%; Score 1301; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 3.4e-109;
Matches 260; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGGAOKLGNVCYF 60
DB 1 MAACRSYKGLVAVITGASGLGATATRLVGGASAVLLDLPNSGGGAOKLGNVCYF 60
QY 61 APADVTSEKDVOTATLAKKGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFOVRLDV 120
DB 61 APADVTSEKDVOTATLAKKGRVDVAVNCAGIAVASKTYNLKKGOTHTLEDFOVRLDV 120
QY 121 NMGTENVIRLVAGEMGQNEPDGQGRVYIINTASVAAFEGOVGAAYASAKGIVGNTL 180
DB 121 NMGTENVIRLVAGEMGQNEPDGQGRVYIINTASVAAFEGOVGAAYASAKGIVGNTL 180
QY 181 PIARDLAPIGIRVMTIAGLFTPLLTSLPEKXANFLASOVPPSRIGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAGLFTPLLTSLPEKXANFLASOVPPSRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

RESULT 3
US-09-931-186-8
Sequence 8, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGRE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REUTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.

APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: wild type ERAB
US-09-931-186-8

Query Match 99.7%; Score 1300; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.2e-109;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
DB 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
QY 61 APADVTSEKDYOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
DB 61 APADVTSEKDYOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
QY 121 NLMGTFNVIKLVAGEMQNEPDGCGRGVYIINTASVAAFEGQVQAAYASASKGIYGMTL 180
DB 121 NLMGTFNVIKLVAGEMQNEPDGCGRGVYIINTASVAAFEGQVQAAYASASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVNFLASQVPPFRIGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVNFLASQVPPFRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEVIKRLDGAIRMOP 261
DB 241 IENPFLNGEVIKRLDGAIRMOP 261

RESULT 4
US-09-931-186-2
Sequence 2, Application US/09931186
Patent No. US20020132319A1

GENERAL INFORMATION:
APPLICANT: ABREO, MELVYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 261
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2

Query Match 99.6%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 5.1e-109;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
DB 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
QY 61 APADVTSEKDYOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
DB 61 APADVTSEKDYOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
QY 121 NLMGTFNVIKLVAGEMQNEPDGCGRGVYIINTASVAAFEGQVQAAYASASKGIYGMTL 180
DB 121 NLMGTFNVIKLVAGEMQNEPDGCGRGVYIINTASVAAFEGQVQAAYASASKGIYGMTL 180
QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVNFLASQVPPFRIGDPAEYAHVQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVNFLASQVPPFRIGDPAEYAHVQAI 240
QY 241 IENPFLNGEVIKRLDGAIRMOP 261
DB 241 IENPFLNGEVIKRLDGAIRMOP 261

RESULT 5
US-09-931-186-4
Sequence 4, Application US/09931186
Patent No. US20020132319A1

GENERAL INFORMATION:

APPLICANT: ABREO, MELVYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPICZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C5V
US-09-931-186-4

Query Match 98.9%; Score 1290; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 3.3e-108;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
DB 1 MAACRSYKGLVAVITGASGLGATAEPLVGGASAVLLDLPNSGGEQAQAKKLGNCVF 60
QY 61 APADVTSEKDYOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120
DB 61 APADVTSEKDYOTLALAKGKFGVDVAVNCAGIAVASKTYNKKGGTHTLEDFORVLDV 120

```
|||||
Db 61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKGQHTLEDFORVLDV 120
QY 121 NMGTNTNRIYVAGENGONEPOGGORGIINTASVAAEQQVGAASASKGIWMTL 180
Db 121 NMGTNTNRIYVAGENGONEPOGGORGIINTASVAAEQQVGAASASKGIWMTL 180
QY 181 PIARDLAPIGIRMTIAPGLFPTLTSPEKVFANFLASQVFPFSLGDPAYAHLYOAI 240
Db 181 PIARDLAPIGIRMTIAPGLFPTLTSPEKVFANFLASQVFPFSLGDPAYAHLYOAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
Db 241 IENPFLNGEYIRLDGAIRMOP 261

RESULT 6
US-09-931-186-6
; Sequence 6, Application US/09931186
; Patent No. US2002013219A1
; GENERAL INFORMATION:
; APPLICANT: ABBEY, MELVYN A.
; APPLICANT: AGREE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAC, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCEYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLARANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HARD2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 6
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C58V
US-09-931-186-6
```

```
Query Match 98.9%; Score 1290; DB 10; Length 261;
Best Local Similarity 99.2%; Pred. No. 3.3e-108;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MAACRSYKGIYAVITGASGLGATPERLVGGASAVLIDLNSGGEAAKXKLNVCYF 60
Db 1 MAACRSYKGIYAVITGASGLGATPERLVGGASAVLIDLNSGGEAAKXKLNVCYF 60
QY 61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKGQHTLEDFORVLDV 120
Db 61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYNLKKGQHTLEDFORVLDV 120
QY 121 NMGTNTNRIYVAGENGONEPOGGORGIINTASVAAEQQVGAASASKGIWMTL 180
Db 121 NMGTNTNRIYVAGENGONEPOGGORGIINTASVAAEQQVGAASASKGIWMTL 180
QY 181 PIARDLAPIGIRMTIAPGLFPTLTSPEKVFANFLASQVFPFSLGDPAYAHLYOAI 240
Db 181 PIARDLAPIGIRMTIAPGLFPTLTSPEKVFANFLASQVFPFSLGDPAYAHLYOAI 240
QY 241 IENPFLNGEYIRLDGAIRMOP 261
Db 241 IENPFLNGEYIRLDGAIRMOP 261
```

```
RESULT 7
US-09-984-245-245
; Sequence 245, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-28
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-245
```

```
Query Match 87.2%; Score 1137; DB 9; Length 227;
```



```

; ORGANISM: Homo sapiens
; US-10-143-090-245
;
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-966-245
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Query Match      87.2%; Score 1137; DB 9; Length 227;
Best Local Similarity 99.6%; Pred. No. 1.5e-94;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 35 ASAVLLDLPNSGGGAQAKKLNCCVFPADYTSKDVOTLALAKKFGGRVDAVNCAGI 94
    |||||
DB 1 ASAVLLDLPNSGGGAQAKKLNCCVFPADYTSKDVOTLALAKKFGGRVDAVNCAGI 60
    |||||
QY 95 AVASKTYNLKKGQHTLEDFOFVLDVNLGTFNVIRLVAGEMQNEPDGQGRVILNTA 154
    |||||
DB 61 AVASKTYNLKKGQHTLEDFOFVLDVNLGTFNVIRLVAGEMQNEPDGQGRVILNTA 120
    |||||
QY 155 SVAAFEQGVQAAVSASAKSGIVGWTLPARDLAPIGIRVMTIAPGLFTPLTSLPEKVA 214
    |||||
DB 121 SVAAFEQGVQAAVSASAKSGIVGWTLPARDLAPIGIRVMTIAPGLFTPLTSLPEKVC 180
    |||||
QY 215 NFLASQVFPSPRLGDPAPETAHVQAIIENPFLNGEVRIDGAIIRMP 261
    |||||
DB 181 NFLASQVFPSPRLGDPAPETAHVQAIIENPFLNGEVRIDGAIIRMP 227
    |||||
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RESULT 10
US-10-143-090-245
; Sequence 245; Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/143,090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
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; ORGANISM: Homo sapiens
; US-10-143-090-245
;
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-966-245
```

```

RESULT 11
US-09-920-923-41
; Sequence 41; Application US/09920923
; Publication No. US2003002273A1
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tszyankov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/09/920,923
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 41
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Flavobacterium sp. R1534
US-09-920-923-41
```

```

Query Match      51.1%; Score 666.5; DB 9; Length 388;
Best Local Similarity 55.5%; Pred. No. 5.8e-52;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;
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QY 8 VGLVAVITGSGSGIGLTAERLVQGGASVLLDLPNSGGGAQAKKLNCCVFPADYTS 67
    |||||
DB 143 IGRVFEVVTGAASGGAASARMLAOGGAKVVIADI-----AEKDADEGAVHAACDVTD 196
    |||||
QY 68 EKDVOITALALAGKFGVADVAVNCAGIIVASKTYNLKKGQHTLEDFOFVLDVNLGTFN 127
    |||||
DB 197 ATAAQGTALATDRGRDLGVLNCGIAPAEEM--LGRDGPRLGDSFRAVATINLIGSFN 254
    |||||
QY 128 VIRLVAGEMQNEPDGQGRVYIINTASVAAFEQGVQAAVSASAKSGIVGWTLPARDLA 187
    |||||
DB 255 MARLAFAAARNEPVR-GERGVIVTASTIAAQDGGIGVAAVAAASGAAGMTLPAROLA 313
    |||||
QY 188 PIGIRVMTIAPGLFTPLTSLPEKVAFLASQVFPSPRLGDPAPETAHVQAIIENPFLN 247
    |||||
DB 314 RIGIRVMTIAPGLFTPLTSLPEKVAFLASQVFPSPRLGDPAPETAHVQAIIENPFLN 373
    |||||
QY 248 GEVIRIDGAIIRMP 261
    |||||
DB 374 GEVIRIDGAIIRMP 387
    |||||
```

```

RESULT 12
US-09-931-186-17
; Sequence 17; Application US/09931186
```

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```
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABREO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENGE, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: THOMPSON, JIM
APPLICANT: THOMPSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-186-17
```

```
Query Match      25.6%; Score 333.5; DB 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 2.8e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
```

```
QY 8 VKGLVAVITGASGLTAEIRLVGQASAVLLDLPNSGGEAOKKL-----GN 56
DB 7 LNSALALVIGAGSGGIRAVSVFLAGEGATVACDIDRAAOETVRLGPGSKGPPGN 66
QY 57 NCVFPAADVTSKEDVQALALAKGKFR-VDVAVNCAGIAVASKTYNKKQCTHTLEDFQ 115
DB 67 HNAF-QADVSEARARCLLEVOACFSRPPSVVASCAGITQDEFLHSE-----DDWD 119
QY 116 RVLNVNMGTFVTLVAGEMQNEPDGQGVIIINTASVAEFEGOVGAAYASAKGI 175
DB 120 KVIAYNLKGTFLVTAQAALVSN-----GCRGSIINSSIVGKGVNGQINYASAKGV 174
QY 176 VGMTPIARDLAPIGIRVWTIAPGLFGTPLTSLPEKVANFLASQVPPSRIGDPAEYAH 235
DB 175 IGLTQTAARELGRHGRCSVLPGRATPMTQKVQKVDKITEIMP-GLHGDEEDVAD 233
QY 236 LVQ--AIIENPFLNGEVTIRLDAIRM 259
DB 234 VVAFLASEDSGYITGTSTVEVTGLPM 259
```

RESULT 13
US-09-815-242-13360
Sequence 13360, Application US/09815242
Patent No. US20020061569A1

```
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
```

```
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13360
LENGTH: 243
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360
```

```
Query Match      25.2%; Score 328.5; DB 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 7.3e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
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```
QY 15 ITGASGLGATAEIRLVGQASAVLLDLPNSGGE-----AQAKLGNVCVAPADVTSE 68
DB 10 ITGSSRGIGLAIHAKRAQAGANIVL-----NSRGALISEBLAESNYGIKVPISGDVDF 65
QY 69 KDVOFLALAKKGFGRDVAVNCAGIAVASKTYNKKQCTHTLEDFQVRLDPAEYAH 128
DB 66 ADKRMIDQAIYALGSDVAVNNAGI--TQDTMLKK---TDADEKVLKVLTAFTNK 119
QY 129 IRVAGEMQNEPDGQGVIIINTASVAEFEGOVGAAYASAKGIYGMTPIARDLAP 188
DB 120 TQSVL-----KPMKMRREGAIIINSSVGLMGNIGQANVAASKAGLIGFTKSVAREVAS 173
QY 189 IGIVMTIAGLGFTPLTSLPEKVANFLASQVPPSRIGDPAEYAHVQAIENPFLNG 248
DB 174 RNINVTIAGMTESDMTALISDKIKETLAQIIP-KEFGQADQVADLTVELAGQDYLTS 232
QY 249 EVIRLDGAIIR 259
DB 233 QVIAIDGSLM 243
```

RESULT 14
US-09-815-242-13581
Sequence 13581, Application US/09815242
Patent No. US20020061569A1

```
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
```


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	Best Local Similarity	32.0%; Pred. No. 1,46-20;	
	Matches	81; Conservative	41; Mismatches 105; Indels 26; Gaps 5;
QY	12	VAVINGGASGGLAAERELUNGOGASAVLLDLPNSGSGAOKKTIQNNVFPAPLVYSEKGV	71
		: : : : : : : : : : : : : : : : : : : :	
Db	4	VCAIFGSGSGIGRAVAQLMARKGYLTIAANLEGASAAAAGDLGDIAPFSCVDAAKEHY	63
		: : : : : : : : : : : : : : : : : : : :	
QY	72	QTALALAKRGFGRDVAVNCAGI-----AVASKTYNNKKGQHTLEDQFQVLDVNMGEF	126
		: : : : : : : : : : : : : : : : : : : :	
Db	64	QNTFEEMEHRLRQVNFVLLVAAGINRDSLIVAKT-----EDMSQLHTNLLGSM	112
		: : : : : : : : : : : : : : : : : : : :	
QY	127	NVIRLVAGEMGQNEPDGQGRGVIIINTASVAFSGQVGOAAYSAKSGGIVGMLPIARDL	186
		: : : : : : : : : : : : : : : : : : : :	
Db	113	LITCKAMRAMIQO-----QGGSIVNVSGIYGLGNSGQGSVYSKSKGLTGFEFRAALAKEV	166
		: : : : : : : : : : : : : : : : : : : :	
QY	187	APGIGRVMTIAPGLFQTPLLTSLPEKVAANFLASQVPPSPRLGDAEVAHYVCAIINPEL	246
		: : : : : : : : : : : : : : : : : : : :	
Db	167	ARKKIVNVYARPEFVITDMTKLKE---HLKNKIPL-GRGGEIIEVAHNVVLLSPFI	222
		: : : : : : : : : : : : : : : : : : : :	
QY	247	NGEYVRLDGAIRK 259	
		: : : : : : : : : : : : : : : : : : : :	
Db	223	TGHVLDVGGDLQ 235	

```

RESULT 17
US-09-823-901-2
; Sequence 2, Application US/09823901
; Patent No. US20020001807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 21509 AND 33770 NOVEL HUMAN
; FILE OF INVENTION: DEHYDROGENASES AND USES THEREOF
; FILE REFERENCE: 1048-036001
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US/09/823,901
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-901-2

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	Query Match	Score 314;	DB 10;	Length 237;
	Best Local Similarity	32.1%;	Pred. No. 1,4e-20;	
Matches	81; Conservative	41;	Mismatches 105;	Indels 26; Gaps 5
QY	12 VAVITGGASGCLALAERLVQGASAVLIDPNSCGEQAOKKLGNNCFAPADVTSEKDY	71		
	: : : : : : : :			
Db	4 YCAITGGSGIGIRAAVQLMARGRIATIAIARNLEAKAAGGLGDHDLAFSCDAKEHY	63		
QY	72 QTALAARGFEGRVVAANCAGI-----AVASKTYNLKKGTHTEDDEFQRYLDVMIGTF	126		
	: : : : : : : : : :			
Db	64 QTPEEMEKHLGRVNFPLVPAAGINDRSLLRKT-----EDWVSQHLTNIJLSM	112		
QY	127 NVIRLVAGEMGNEDDQGRVILINTASVAFBEQVGGAASAKGVIGMTLLIARLP	186		
	: : : : : : : : : : :			
Db	113 LTCKAMRAMIQO-----QQGSIVNVGSIYVLKGNGSGSVTSASRGGLVGRSRMLAKCV	166		
QY	187 APGIRVMTADFGPTLLTSPERKANFTLASOVFPFSRLDPAPAYALTVOALINENPL	246		
	: : : : : : : : : :			
Db	167 ARKKIRVVNAVADGPFVHTDKTLKEE--HKKNIPL-QRGSETIEVAHAVVFLESPTY	222		
QY	247 NGEVIRLDGARIM	259		
	: : : : :			
Db	223 TGHVLVVDGGLQI	235		

RESULT 18
US-09-931-186-15
: Sequence 15 Application US/09931186

```

? Patent No. US20020132319A1
? GENERAL INFORMATION:
? APPLICANT: ABREO, MELWYN A.
? APPLICANT: AGREE, CHARLES S.
? APPLICANT: AUST, ROBERT
? APPLICANT: KISSINGER, CHARLES R.
? APPLICANT: MARGOSIAR, STEVE
? APPLICANT: MENG, JERRY J.
? APPLICANT: PELLETIER, LAURA A.
? APPLICANT: REJTO, PAUL A.
? APPLICANT: SHOWALTER, RICHARD E.
? APPLICANT: TEMPCZYK-RUSSELL, ANNA
? APPLICANT: THOMSON, JIM
? APPLICANT: VANDERPOOL, DARIN
? APPLICANT: VILLARANCA, J. ERNEST
? TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
? TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
? TITLE OF INVENTION: OF INHIBITORS THEREOF
? FILE REFERENCE: 0125-0049
? CURRENT APPLICATION NUMBER: US/09/931,186
? CURRENT FILING DATE: 2001-08-17
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 15
? LENGTH: 253
? TYPE: PRT
? ORGANISM: Steptomyces hydropneumans
? US-09-931-186-15

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	Query Match	23.7%	Score 308.5;	DB 10;	Length 253;
	Best Local Similarity	33.3%;	Pred. No. 4.8e-20;		
	Matches	84;	Conservative 48;	Mismatches 101;	Indels 19; Gaps 7;
Qy		8 VKGLVAVITGGASGIGLATAERLVGGOGASAVALLDIPNSGEQDAKKLGNNCFVAPADYTS	67		
	:	: : : : : : : : : : : : : : : : : : : :			
Db		3 LSGTIVITITGGARGIGLEAARQAQAAAGRVVLADVLDKEGAATARELDDAARYOHLDTYTI	62		
Qy		68 EKDVTOTALAKKRGKGRVDVAVNCAGIIVASKTYLKKGQHTLEDPCRYALDVNLMGFEN	127		
	:	: : : : : : : : : : : : : : : : : : : :			
Db		63 FEDMQRYAYAREEGSGVDLGNNAISTGMFL-----ETESVERFRKYVEINLTGVFI	116		
Qy		128 VIRLVAGMGONEPDQGQGVIIINTASVAAEFGVGQAANSASKSAGGIYGMTLPRLARDLA	187		
	:	: : : : : : : : : : : : : : : : : : : :			
Db		117 GMKTATPAM---KTAGS--GSIVNISSAAGIMGTALTSSYGASKSWSVGYSKLAAVELG	170		
Qy		188 PIGIKVMNIAPGLFETPLL--TSLDEKANFTLASQVPPPSRRLQGPFAEVAHNLQVALTE--N	243		
	:	: : : : : : : : : : : : : : : : : : : :			
Db		171 TDRIRVNSVHRGMTPTPTMTAETGRINQBGNT--PRTPM-GRVGEPEGIAGAVVKLLSDTS	227		
Qy		244 PFNLGEVTRLDG	255		
	:	: : : : : : : : : : : : : : : : : : : :			
Db		228 SVYTGAELAVDG	239		

```

/ RESULT 19
/ US-09-479-040-9
/ Sequence 9, Application US/09479040
/ Publication No. US20020182690A1
/ GENERAL INFORMATION:
/ APPLICANT: MCCOOL, Gabriel J.
/ APPLICANT: Cannon, Maura C.
/ APPLICANT: Cannon, Francis C.
/ APPLICANT: Valentin, Henry E.
/ APPLICANT: Guys, Kenneth J.
/ TITLE OF INVENTION: POLYHYDROXYALKANOATE BIOSYNTHESIS ASSOCIATED PROTEINS
/ TITLE OF INVENTION: AND CODING REGION IN BACILLUS MEGATERIUM
/ FILE REFERENCE: M087212
/ CURRENT APPLICATION NUMBER: US/09/479,040
/ CURRENT FILING DATE: 2000-01-07
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 9
/ LENGTH: 247

```


TYPE: PR
ORGANISM: Bacillus megaterium
US-09-479-040-9

Query Match 23.2%; Score 303; DB 9; Length 247;
Best Local Similarity 29.1%; Pred. No. 1.5e-19;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVNGIYAVITGASGIGLTAERLVGQ-----ASAVLLDLPNSGGGAQAK 53
DB 3 TLGGKVAIVGSGKSGAATRELASNGKVAVAVNNSKESAEATVKEIKDNGEA---- 58
QY 54 LGNNCFAPADVTSEKDVOTALAKGKGRVDVAVNCAGIAVASKTYNLRK-GQTHLE 112
DB 59 -----IAYQADVYVQAKHLIETKAARQGLILVNNNGI---TRDRSFKLGE-----E 106
QY 113 DFOQVLDVNLMTFNVIRLVAGEMQNEPDGQROVYIINTASVALEFGVQGAAYSASK 172
DB 107 DMKKVIDVNLHSYNTTSAALTLLESE---GGR---VINISIIQAGGFGQTNISAK 160
QY 173 GGIYGTLPFARDLAPIGIRVMTIAPGLFTPLLSPEKVANFLASQVPPSRLGDPAE 232
DB 161 AGHLGFTKSLALELAKTGVVNAICPGFITEENVMAIPEDVRKIVAKIP-TRLGHAHE 219
QY 233 YAH-LVQAITEENPLNGEVIRLDGAIRM 259
DB 220 IARGVVIARDGAVITGQOLNIGLYM 247

RESULT 20

US-09-773-748-1
Sequence 1, Application US/09773748
Publication No. US20020187537A1

GENERAL INFORMATION:
APPLICANT: Wada, Masaru
TITLE OF INVENTION: Levodione reductase gene and use thereof
FILE REFERENCE: Levodione reductase
CURRENT APPLICATION NUMBER: US/09/773,748
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: EP00101665.8
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 267
TYPE: PR
ORGANISM: Corynebacterium aquaticum
US-09-773-748-1

Query Match 22.8%; Score 297.5; DB 9; Length 267;
Best Local Similarity 32.2%; Pred. No. 5.1e-19;
Matches 85; Conservative 45; Mismatches 97; Indels 37; Gaps 9;

QY 12 VAVITGASGIGLTAERLVGQASAVLLDLPNSGGGAQAKKGNCFAP-----ADVT 66
DB 15 VVLTGGSSGGRATAVRLAEGAKLSLVSSSEGLASRAAVLETPADEVLTVDVS 74
QY 67 SEKDVTALALAKGFRGVAVVAVNCAGIAVASKTYNLRKQTHLEDFORVLDVNLMTF 126
DB 75 DEAGVEAVYATATRFGRIDGFEFNAGIEGQ-----NPRESFAAEFDKVSINLGEV 129
QY 127 ----NVRILVAGEMQNEPDGQROVYIINTASVALEFGVQGAAYSASKGIYGTLP 182
DB 130 LGLEKVIKIMR-----EAGS---GAVVNTASVGIIRGIGNSGVIAAHGVAGLRNS 179
QY 183 ARDLAPIGIRVMTIAPGLFTPLLS-----PEKVA-NFLASQVPPSRLGDPAEY 233
DB 180 AVEGRGIRINATLAPGLVTPVNVENSKQDLPNPKAAEEF---GVNSKRGGEAPEI 237
QY 234 AHLVQAITEEN--PFLNGEVIRLDG 255
DB 238 AAVVAFLLSDDSAYVNAIVVPIDG 261

RESULT 21
US-10-307-385-6
Sequence 6, Application US/10307385
Publication No. US2003007797A1

GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZAKI, KENZO
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/10/307,385
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US/09/363,189
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PR
ORGANISM: Gluconobacter oxydans
US-10-307-385-6

Query Match 22.7%; Score 296.5; DB 9; Length 262;
Best Local Similarity 32.0%; Pred. No. 6.1e-19;
Matches 87; Conservative 41; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVKGIYAVITGASGIGLTAERLVGQASAVLLDLPNSG---GEAQAARKGNCFAP 62
DB 3 KRFNGKVLVTGAGNIGLTAFLRLAEGTALALLDMRLEKAEAVRREKVEARVY 62
QY 63 ADVTSEKDVOTALALAKGFRGVAVVAVNCAGIAVASKTYNLRKQTHLEDFORVLDVNL 122
DB 63 CVTSEENVITGVDSVVRDFGKIDFLFNAGYGA-----FAPVDYPSDFARVLTIV 117
QY 122 MGFNVIRLVAGEM-GONEPDGQROVYIINTASVALEFGVQGAAYSASKGIYGTLP 181
DB 118 TCAFVHLKAVSKOMITON-----YGRVNTASAGVKGPPNNMAVYASGAILALLET 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GIPLTLSPEKVANFLASQVPPS 225
DB 171 AALDLAPYINIRVNAISPYGMPFMEWROVELQAKVGSQYESTDKVVAQOMIGSPV-R 229
QY 226 RLGDDPAEYVHLVQAITE--ENPLNGEVIRLDG 255
DB 230 RYGDINEIRGVVAFLLGDSSPTMGVNLPIAG 261

RESULT 22

US-09-802-853-6
Sequence 6, Application US/09802853
Patent No. US20010034049A1

GENERAL INFORMATION:
APPLICANT: SUGIYAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SHUNICHI
APPLICANT: YOKOZAKI, KENZO
TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1024-0
CURRENT APPLICATION NUMBER: US/09/802,853
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 09/363,189
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP10-216047
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 262
TYPE: PR

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ORGANISM: Gluconobacter oxydans
us-09-802-853-6

Query Match 22.7% Score 296.5; DB 10; Length 262;
Best Local Similarity 32.0%; Pred. No. 6, 1e-19;
Matches 87; Conservative 41; Mismatches 109; Indels 35; Gaps 7;

QY 6 RSVKGLAVITGGASGLGATIRLVGGASAVLIDFNSG---GEOAKRLGNKCYFAP 62
DB 3 KKFNGKVLTVGAGGNIGATLRLAEGTIALIDMNRREALERKASRVEARSYV 62
QY 63 ADVSEKDVQTLALAKGFGVDVAVACAGIAVASKTYNKKGGTHLEDFORVLDVNL 122
DB 63 CVTSEAVITGVDSVADFGKIDLFNNAGYGA-----FAPVDYPSDDFARVLTINV 117
QY 123 MGTENVIRLVAGEM-GQNEPDGGGQGVYINTASYAATEGOVGAAYSASRGIVGMTLP 181
DB 118 TGAFTVLKAVSRQMTTON-----YGRIVTVASMAVGKGPNNMAAGASGAILTRET 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GTPLLTSLPEKVAANFLASGVPPS 225
DB 171 AALDLAPYIRVNAISPGIMSGPFMRQVELQAKVSGQYFTDPKVVAAQDMISGVP-R 229
QY 226 RLGDPAEYAHVQAIT--ENPLNGEYIRLDG 255
DB 230 RYGDINEIPGVAVAFLLGDDSSFMGTGNLPIAG 261

RESULT 23
US-09-978-295A-468
Sequence 468, Application US/09978295A
Patent No. US2002015606A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Iyar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819

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PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 22.5%; Score 293.5; DB 9; Length 270;
Best Local Similarity 32.7%; Pred. No. 1,2e-18;
Matches 86; Conservative 42; Mismatches 114; Indels 21; Gaps 8;

1 MAACRSYKGLVAVITGASGLGLATAERLVGOGASAVLLDIPNSGGEAKKLGNNVF 60
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QY 121 NLMTFNVIRLVAGENGONPPDGGGGRVYIINTASVAEFGVGAAYASKGGIVGKTL 180
DB 114 NLGTVYLTALPLPYLRKSO-----GNVINTSLVGAIGQAVPYATKAVATMK 166
QY 181 PIARDLPIGRMTTAPGFGPLLSL-----PEKAVNLAQVFP-SRIGDPAEY-A 234
DB 167 ALADESPYGVNRNCSPGIMTPLEWELALMPDRATIRSGMLQPIGRMGQPAEVA 226
QY 235 HLYOAIENPPLNG-EVIRLDGA 256
DB 227 AAVFLASEANFCGIELLVGA 249

RESULT 25
US-09-978-192A-468
Sequence 468, Application US/09978192A
Patent No. US2002017753A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT FILING DATE: 2001-10-15
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Query Match 22.5% Score 293.5; DB 9; Length 270;
Best Local Similarity 32.7% Pred. No. 1.2e-18;
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1 MAAARSRKGLVAVITGASGLATAEELVGGASAVLIDLPNSGGEAKKGNVCF 60
1 MATGTR-YAKGVVYVGGGIGAGIYRAVNSGARVYIDCKDSGSALECEL-PGAYF 58
61 APADVTSEKVOYRALALAKRGKRVYAVVACAGIAVASKYNNKKOTHTLEPCVAVLV 120
59 ILCDVTEDDVYKTLVSETIRFRGLDCVNNAGHPPP-----QREBTSAGCFRDLLEL 113
121 NLMGTFVIRLVAGEMGNPDGGRGVITNTASVAEFGVGGCAAYSASKGIYGMTL 180
114 NLCTYTLTKALPYLRKSQ-----GNVINISLVGALGQAQAVPYATKCAVTAMTK 166
181 PIADLAPIGIRVWTIPAGLFGTPLTSL-----PEKIANPLASQVPPP-SRDDPAYF-A 234
167 ALALDESPYGRVACISPGNIMTWPLWELALAMPDPATIREGMLAQPIRGMQPAVEGA 226
235 HLYQATIEENPLNG-EVIRLDGA 256
227 AAVFLASEANFCIGIELLVITGGA 249

Search completed: June 23, 2003, 14:59:49
Job time : 22.333 secs

Thu Jun 26 06:55:04 2003

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Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:23:47 ; Search time 15.6667 Seconds
(without alignments)
1601.559 Million cell updates/sec

Title: US-09-931-186-20

Perfect score: 1304

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Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750	57.5	258	2	T20484 hypothetical prote
2	722	55.4	255	2	H83326 probable short-cha
3	713	54.7	255	2	AG3611 3-oxoacyl-(acyl)-ca
4	673.5	51.6	250	2	H40554 probable dehydroge
5	672	51.5	255	2	H95360 probable imported
6	644	49.4	257	2	F97531 probable short-cha
7	644	49.4	257	2	AG2750 3-hydroxyacyl-CoA
8	597	45.8	260	2	C87264 3-hydroxyacyl-CoA
9	382.5	29.3	247	2	E70740 probable fabg2 pro
10	355	27.2	252	2	F83098 probable short-cha
11	345.5	26.5	249	2	F97338 3-ketoacyl-acyl-ca
12	343	26.3	246	2	H72219 3-oxoacyl-(acyl)-ca
13	335.5	25.7	246	2	C83961 3-oxoacyl-(acyl)-ca
14	335.5	25.7	297	2	T51084 3-oxoacyl-(acyl)-ca
15	335	25.7	320	2	S22450 3-oxoacyl-(acyl)-ca
16	334.5	25.7	251	2	AH2042 3-oxoacyl-(acyl)-ca
17	332	25.5	246	2	H84136 3-oxoacyl-(acyl)-ca
18	330.5	25.3	248	2	F82128 3-oxoacyl-(acyl)-ca
19	328.5	25.2	243	2	E97919 3-oxoacyl-(acyl)-ca
20	328.5	25.2	260	2	T36846 probable dehydroge
21	327.5	25.1	243	2	C69508 3-oxoacyl-(acyl)-ca
22	326.5	25.0	243	2	F86721 hypothetical prote
23	317	24.3	243	2	D90481 hypothetical prote
24	316.5	24.3	259	2	H98137 3-oxoacyl-(acyl)-ca
25	316.5	24.3	259	2	A13149 3-oxoacyl-(acyl)-ca
26	315.5	24.2	260	1	A48154 short-chain alcoh
27	315.5	24.2	296	2	E87260 hypothetical prote
28	313.5	24.0	240	2	H75014 3-oxoacyl-(acyl)-ca
29	313.5	24.0	247	2	S77280 3-oxoacyl-(acyl)-ca
30	313	24.0	247	2	F82776 3-oxoacyl-(ACP) re
31	313	24.0	252	2	AB3545 toluenesulfonate z
32	311.5	23.9	244	2	AB0195 3-oxoacyl-(acyl)-ca
33	311.5	23.9	246	2	AB9621 3-oxoacyl-(acyl)-ca
34	310	23.8	256	2	A10406 probable dehydroge
35	310	23.8	267	2	T11579 probable short cha
36	309	23.7	249	2	AG3121 dehydrogenase Atu4
37	309	23.7	253	2	H98165 3-oxoacyl-(acyl)-ca
38	305.5	23.4	247	2	AG1300 3-ketoacyl-acyl-ca
39	305	23.4	260	2	H70758 probable fabg3 pro
40	303.5	23.3	247	2	AG1672 3-ketoacyl-acyl-ca
41	303	23.2	248	2	H98258 3-oxoacyl-(acyl)-ca
42	303	23.2	248	2	A13025 3-oxoacyl-(acyl)-ca
43	302	23.2	255	1	S39737 glucose 1-dehydrog
44	302	23.2	255	1	S10707 20beta-hydroxyster
45	300.5	23.0	258	2	C70885 probable dehydroge
46	300.5	23.0	296	2	T26723 hypothetical prote
47	300	23.0	250	1	S47054 probable dehydroge
48	300	23.0	252	2	B90495 hypothetical prote
49	298	22.9	255	2	H84288 3-oxoacyl-(acyl)-ca
50	297	22.8	265	2	T36396 probable short cha
51	296	22.7	245	2	AE3517 3-oxoacyl-(acyl)-ca
52	293.5	22.5	244	2	T12051 3-oxoacyl-(acyl)-ca
53	293	22.5	258	2	D95284 probable imported
54	292.5	22.4	248	1	H70447 3-oxoacyl-(acyl)-ca
55	292	22.4	249	1	B37762 bile acid 7-dehydr
56	292	22.4	272	2	AG3359 3-oxoacyl-(acyl)-ca
57	291.5	22.4	244	1	B42147 short-chain alcoh
58	289.5	22.2	303	2	T46064 3-oxoacyl-(acyl)-ca
59	288.5	22.1	244	2	C90812 3-oxoacyl-(acyl)-ca
60	288.5	22.1	244	2	C85672 3-oxoacyl-(acyl)-ca
61	288	22.1	263	2	AB0812 probable oxidoredu
62	287.5	22.0	246	1	RDALAE acetoacetyl-CoA re
63	287.5	22.0	254	1	G75333 3-oxoacyl-acyl car
64	285.5	21.9	244	2	AD0642 3-oxoacyl-(acyl)-ca
65	285.5	21.9	257	2	A72395 oxidoreductase, sh
66	285	21.9	255	2	C82644 2,5-dichloro-2,5-c
67	284.5	21.8	253	2	B86737 acetoaldehyde dehydrogen
68	284.5	21.8	256	2	E72477 hypothetical prote
69	284.5	21.8	272	2	A99950 acetoacetyl-CoA re
70	283.5	21.7	246	1	DEKCMG acetoaldehyde dehydrogen
71	283	21.7	258	2	B89773 acetoaldehyde dehydrogen
72	282.5	21.7	521	2	C87474 hypothetical prote
73	281.5	21.6	248	2	B81695 3-oxoacyl-(acyl)-ca
74	281	21.5	255	2	D72377 oxidoreductase, sh
75	281	21.5	260	2	F82954 probable short-cha
76	279.5	21.4	241	1	S06998 acetoacetyl-CoA re
77	279	21.4	240	1	F87312 acetoacetyl-CoA re
78	279	21.4	262	2	B97588 oxidoreductase, sh
79	279	21.4	262	2	AG2809 short chain dehydr
80	278.5	21.4	289	2	D69835 glucose 1-dehydrog
81	277	21.2	246	1	B99279 acetoacetyl-CoA re
82	276.5	21.2	248	1	B87223 probable 3-ketoacy
83	276.5	21.2	286	2	G63378 probable short-cha
84	276	21.2	249	1	A11841 bile acid dehydrox
85	276	21.2	259	2	E95903 glucose 1-dehydrog
86	276	21.2	263	2	S01237 glucose 1-dehydrog
87	276	21.2	267	2	B87578 hypothetical prote
88	276	21.2	285	1	A65017 probable 3-oxoacyl
89	276	21.2	285	2	A10101 probable oxidoredu
90	276	21.2	285	2	DB5885 probable oxidoredu
91	275.5	21.1	248	2	T44361 acetoacetyl-CoA re
92	275	21.1	319	2	S22416 3-oxoacyl-(acyl)-ca
93	274.5	21.1	244	2	T44444 3-oxoacyl-(acyl)-ca
94	272.5	20.9	240	2	S75021 3-ketoacyl-acyl-ca
95	272.5	20.9	241	2	A12916 acetoacetyl-CoA re
96	272.5	20.9	245	2	D97691 acetoacetyl-CoA re
97	272.5	20.9	248	2	F71538 probable 3-oxoacyl
98	272.5	20.9	262	2	S02259 glucose 1-dehydrog
99	272	20.9	251	2	G72389 oxidoreductase, sh
100	271.5	20.8	246	2	B89886 3-oxoacyl-(acyl)-ca

EMBL: M15813; AAB61153.1; -
 DR PIR: A28212; A28212.
 DR PIR: A26938; A26938.
 DR PIR: B37762; B37762.
 DR HSP; P19992; IHD.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Oxidoreductase; NAD, Bile acid catabolism; Multigene family.
 FT NP_BIND 7 13 NAD (POTENTIAL).
 FT NP_BIND 32 36 NAD (POTENTIAL).
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT CONFLICT 159 162 TSRA -> IQSG (IN REF. 2).
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Query Match 22.4%; Score 292; DB 1; Length 249;
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 DB 58 EVLG----FAP-DLTSRDVMAAVGTAAQKGRLDVIMNNGITMNGVFSVSE----- 106
 OY 112 EDFQRYLDVNLMTFNVIRLVAGEKQNEPDQSGRGVITNTASVAAFEQGVGAAYAS 171
 DB 107 EDFKIMDINVGAFN-----GMSAYQCKMDKOGVITNTASTVGTIGSLGIGYPTS 160
 OY 112 KGIYVMTLPFARADAPFIRGIVMTAPGLFGPLTSLPEVAVNFASQVFPRLDPA 231
 DB 161 KAGVIGLTHGLREIRKININVGAFVAVTIDMTKGLPRILLDYLTLPK-RMLKPE 219
 OY 232 EYALHVAITENPFLNG---EYIRIDGAIR 258
 DB 220 EIAN-VYFLASDLASGITATTISVDGAYR 248

RESULT 21

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AC P25716; P78221;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-l-acyl-carrier protein reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 GN FABG OR B1093.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL J. Biol. Chem. 267:5751-5754(1992).

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 RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horinouchi T.;
 RA "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."
 RT DNA Res. 3:137-155(1996).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-l-acyl-carrier protein + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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 CC
 DR EMBL: M84991; AAA23739.1; -
 DR EMBL: AB000210; AAC74177.1; -
 DR EMBL: D90745; BAA35901.1; -
 DR PIR: B42147; B42147.
 DR HSP; P29132; IDEI.
 DR ECGene: EG11318; fabG.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 151 151 NADP (BY SIMILARITY).
 FT CONFLICT 30 30 A -> G (IN REF. 1).
 SQ SEQUENCE 244 AA; 25560 MW; 48EC1F2A7FEEDFD CRC64;

Query Match 22.4%; Score 291.5; DB 1; Length 244;
 Best Local Similarity 30.0%; Pred. No. 1.0e-15;
 Matches 76; Conservative 50; Mismatches 112; Indels 15; Gaps 4;

OY 9 KGLVAVITGGASGIGLTAERLYVGQASAVLLDLPNSGEPAQAKKLGNNCFAPADVTSE 68
 DB 4 EGRALVYTGASRGGRALAEFLAARGAKVIGTATSENGAQAISDYLGANGKGLMVTDP 63
 OY 69 KDVOATLALAKKGRGRVDVAVNCAGIYVASKTYMLKGGHTLEDPQRYLDVNLMTFNV 128
 DB 64 ASIESVLEKTRAERGEVDILVNNAGITRDMLNRMD-----EENWDITELSSVERL 117
 OY 129 IRLVAGEKQNEPDQSGRGVITNTASVAAFEQGVGAAYASAGSGIVGWTLPFARADAP 188
 DB 118 SKAYMRAMMK-----RHGRITIGSVYVTMNGGANGAANAAGLIGFSKSLAEVAS 171
 OY 189 IGRVMTIADGLFGTLPPLTSLPEKAVNFASQVFPRLDPAEYALVO--AITENPFL 246
 DB 172 RGIYVAVVAPGFETIDTRALSDQRFAGILAYVP-AGRLGAQEDIANAVAFILASDEAYI 230
 OY 247 NGEYIRLDGAIRM 259
 DB 231 TGETLVHNGGMYM 243

RESULT 22

UCPA_SALTY STANDARD; PRT; 263 AA.
 ID UCPA_SALTY
 AC B37471

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Db 116 RMSRAVLRGMKK-----RAGRIIVGSGVYGMNGNAGOTNYAAAKAGVIGFTKSMREV 169
Qy 187 APIGIRVMTIAPGLFGTPLLTSLEPKVANFLASQVPPSRIGDPAEYAHLV--QATLENP 244
Db 170 ASRGVTVNVAAPGLEIDMTKALNDQRAATLSNVP-AGRLGDREIASAVFLASPEAA 228
Qy 245 FLNGEYIRLDGAIKM 259
Db 229 YITGETLHVNGMYM 243

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RESULT 19

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FABG_AQUAE STANDARD: PRT: 248 AA.
ID 06/610:
AC 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
GN acyl carrier protein reductase).
OS FABG OR AQ.1716.
OC Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_Taxid=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RA MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Grahman D.E., Overbeek R., Sneed M.A., Keller M., Aubay M., Huber R.,
RA Grelman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RT Nature 392:353-358(1998).
RL

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CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NAD(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
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CC
CC
CC EMBL: AE000752; AAC07575.1; -
DR HSSP: P50163; ZAE1.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT.1.
KM Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 12 36 NADP (BY SIMILARITY).
FT ACT_SITE 157 157 BY SIMILARITY.
SQ SEQUENCE 248 AA; 26867 MW; 5CED9EB9AD83FE2C5 CRC64;

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Query Match 22.4%; Score 292.5; DB 1; Length 248;
Best local similarity 30.0%; Pred. No. 1.4e-15;
Matches 77; Conservative 50; Mismatches 109; Indels 21; Gaps 6;
Qy 8 VKLVAVITGGASGLIATRAERLVGGASAVLLDLPNSGGEAQAQKLVG-----NCFARA 63
Db 5 LQKVSILVGTSTGIGRAIAEKIASAGSVITITGSGEAKAVAEIANKYGVKAHGVEM 64
Qy 64 DVSEKDVQCTALALAKGKRGVAVNVCAGIAVASKTYNMLKKGQETLLEDFORVLDVNLK 123

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Qy 124 GFENVIRLVAGEGMONEPDGGOR-GVITNTASVAFAEGOVGAAYSAKSGIVGTLPI 182
Db 119 GFELVYONSIRKIK-----QRMORIVNISSVGFTEVNCQVNTSTKALIGFTKSL 171
Qy 183 ARDLAPIGIRVMTIAPGLFGTPLLTSLEPKVANFLASQVPPSRIGDPAEYAHVQAITE 242
Db 172 AKELAPRNVLNVNVAAPGLEIDMTAVLSEIKQKYEQIPL-GREGSPREAVANVYLQCS 230
Qy 243 N--PFLNGEYIRLDGAI 257
Db 231 ELASITGEYIVHNGM 247

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RESULT 20

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BA71_EUBSP STANDARD: PRT: 249 AA.
ID BA71_EUBSP
AC P07914;
DT 01-AUG-1988 (Rel. 08, Created)
DI 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) (Bile acid
DE 7-dehydroxylase) (7-alpha-HSDH) (Bile acid-inducible protein).
GN BA71 AND BA73.
OS Eubacterium sp. (strain VPI 12708).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_Taxid=29347;
RN [1]
RP SEQUENCE FROM N.A. (BA73).
RA MEDLINE=90330548; PubMed=2376563;
RA Gopal-Srivastava R., Mallonee D.H., White W.B., Hylemon P.B.;
RT "Multiple copies of a bile acid-inducible gene in Eubacterium sp.
RT strain VPI 12708."
RT J. Bacteriol. 172:4420-4426(1990).
RL

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CC [2]
CC SEQUENCE FROM N.A. (BA71), AND SEQUENCE OF 1-33.
CC
CC MEDLINE=88197993; PubMed=2834320;
CC Coleman J.P., White W.B., Lijewski M., Hylemon P.B.;
CC "Nucleotide sequence and regulation of a gene involved in bile acid
CC 7-dehydroxylation by Eubacterium sp. strain VPI 12708."
CC J. Bacteriol. 170:2070-2077(1988).
CC
CC
CC [3]
CC SEQUENCE OF 1-55 FROM N.A. (BA71), AND SEQUENCE OF 1-33.
CC
CC MEDLINE=87165759; PubMed=3549693;
CC Coleman J.P., White W.B., Hylemon P.B.;
CC "Molecular cloning of bile acid 7-dehydroxylase from Eubacterium sp.
CC strain VPI 12708."
CC J. Bacteriol. 169:1516-1521(1987).
CC
CC -1- FUNCTION: 7-ALPHA-DEHYDROXYLATION OF CHOLIC ACID, YIELDING
CC DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST
CC AFFINITY WITH TAUROCHENOXYCHOLIC ACID.
CC -1- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-
CC cholanoate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-
CC cholanoate + NADH.
CC -1- PATHWAY: Bile acid catabolism.
CC -1- INDUCTION: PRESENCE OF C(24) BILE ACIDS CONTAINING A
CC 7-ALPHA-HYDROXY GROUP.
CC -1- SIMILARITY: THERE ARE THREE GENES FOR BILE ACID PROTEINS: BA71 IS
CC IDENTICAL TO BA73 AND THERE IS 81% IDENTITY WITH BA72.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
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CC
CC EMBL: M34658; AAB61155.1; -

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QY 239 AITF--NPFLNGEYRLDGAIRMQ 260
 Db 232 FLASDLSSYMTGSATTAAGGYTAQ 255

RESULT 17

YAVI_RHISN STANDARD; PRT: 548 AA.

AC Q53217;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative short-chain type dehydrogenase/reductase YAVI (EC 1.1.1.100).
 GN YAVI.
 OS Rhizobium sp. (strain NGR234).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group.
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97305956; PubMed=9163424;
 RA Freberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RT "Molecular basis of symbiosis between Rhizobium and legumes."
 RL Nature 387:394-401(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96389014; PubMed=8796346;
 RA Freberg C., Perret X., Broughton W.J., Rosenthal A.,
 RT "Sequencing the 500-kb GC-rich symbiotic region of Rhizobium sp.
 NGR234 using dye terminators and a thermostable 'sequenase': a
 RT beginning."

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z68203; CAA92424.1; ALT_INIT.
 DR EMBL: AE000101; AAB91897.1; -
 DR HSSP: P50163; ZAE1
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 2.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Hypothetical protein; Oxidoreductase; Plasmid; Repeat;
 KM Multifunctional enzyme.
 FT DOMAIN 1 250
 FT DOMAIN 2 250
 FT NP_BIND 12 548
 FT NP_BIND 12 548
 FT ACT_SITE 154 154
 FT ACT_SITE 154 154
 FT NP_BIND 280 304
 FT NP_BIND 280 304
 FT ACT_SITE 420 420
 FT ACT_SITE 420 420
 SQ SEQUENCE 548 AA; 57593 MW; 399598C5DF17C23F CRC64;

Query Match 22.74; Score 296.5; DB 1; Length 548;
 Best Local Similarity 33.6%; Pred. No. 1.7e-15;
 Matches 86; Conservative 40; Mismatches 101; Indels 29; Gaps 8;

QY 10 GLVAVITGGASGLATATERTLVGOGASAVLLDLPNSGGEAQAQKLGNNCVFAPADYTSK 69
 Db 9 GRVIVVTGAAGSIGRALVDIFANGDVVAVVADLPDPSGVIELGQNLCEPHLGEVDVSRED 68

QY 70 DVCATATLAKGKRGKRDVAVNCGI-----AVASKTYNKKGGQTHLEDFORVLDVNLNGTE 125
 Db 69 DVVALRLLEKRRSRLEVLNVNNGIGPPTMAATADT-----ALEDFORALATLVGA 119

QY 126 FNVIKRLVAGEMGQNEPDGQGRGVITINTASVAFAEGOVGQAASAKSGIYKTLPIARD 185
 Db 120 YSVACETIAKLM-----KRG-----AAIVVASLADLLGNPKRSATAAKAGLITSTKSLAOR 171
 QY 186 LAPIGIRKMTIAPGLFETPLITSLPERVANE-----IASQVPPPSRLGDPATYAHLYQ--A 239
 Db 172 WASRGIRVAVAGCHVPTPVAAEL-ERACKLDVSAIRRRVPL-GRIRAPDEIRAAVAFILA 229
 QY 240 ILENPFLNGEYRLD 255
 Db 230 SAQASITTGSTLYVDG 245

RESULT 18

FABG_VIBHA STANDARD; PRT: 244 AA.

AC P55336;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 GN FABG.
 OS Vibrio parvulus.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B392;
 RX MEDLINE=96134997; PubMed=8550484;
 RA Shen Z., Byers D.M.;
 RT "Isolation of Vibrio parvulus acyl carrier protein and the fabg, acpp,
 RT and fabf genes involved in fatty acid biosynthesis."
 RL J. Bacteriol. 178:571-573(1996).
 CC CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SCR) FAMILY.
 CC -----
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 CC -----
 CC EMBL: U39441; AAC43589.1; -
 DR HSSP: P19992; IHDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP.
 FT NP_BIND 10 34
 FT NP_BIND 10 34
 FT ACT_SITE 151 151
 FT ACT_SITE 151 151
 SQ SEQUENCE 244 AA; 25519 MW; FC41A1C65B8CDAAA CRC64;

Query Match 22.5%; Score 293.5; DB 1; Length 244;
 Best Local Similarity 29.8%; Pred. No. 1.1e-15;
 Matches 76; Conservative 51; Mismatches 113; Indels 15; Gaps 4;

QY 7 SVKGLVAVITGGASGLATATERTLVGOGASAVLLDLPNSGGEAQAQKLGNNCVFAPADYTSK 69
 Db 2 NLEGRKIALVTVGASRIGALIELLVERGATVIGTATSEGGAAALSEYLGENGKGLATNV 61
 QY 67 SEKDVQATLALAKGKFGSDVAVNACAGIAVASKTYNKKGGQTHLEDFORVLDVNLNGTE 126
 Db 62 DVESEIATLTKINDECGAIDLIVNNAIGTRNLMRKD-----DEMNDIINTNLTPIY 115
 QY 127 NVIRLVAGEMGQNEPDGQGRGVITINTASVAFAEGOVGQAASAKSGIYKTLPIARD 186

Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
 -1- CATALYTIC ACTIVITY: Androstane-3-alpha,17-beta-diol + NAD(+) = 17-beta-hydroxyandrostane-3-one + NADH.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
 DR PIR: S10707, S10707.
 DR PDB: 2HSD, 31 AUG 94.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Oxidoreductase; NAD: Steroid metabolism; 3D-structure.
 FT NP_BIND 10 34 NAD (BY SIMILARITY).
 FT ACT_SITE 152 152
 SQ SEQUENCE 255 AA; 26484 MW; 9CB93CB66A628D5 CRC64;
 Query Match 23.2%; Score 302; DB 1; Length 255;
 Best Local Similarity 33.6%; Pred. No. 2,7e-16;
 Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;
 QY 8 VKGLAVITGASGLATPRLVYVGVGASAVLLDIPNSGDAQAKKGNCCVAPADYTS 67
 DB 4 LSGKTVITGARGIGAEARQAQAVAGARVVLADVLEDEGAATARELDGAARYOHLDTYI 63
 QY 68 EEDVGTALAKGKRGVAVNCAGIYASVSKTYLKKGGHTLEDFOFVLDVNLGTFEN 127
 DB 64 EEDMORVAVYAREEGSYDGLVNNAGISTGFL-----EHSVRFKRYVDINLTGYFI 117
 QY 128 VTRVAGENGQNEPDGQGVYIINTASVAAFEQGVGAQVSAKSGIVGTLPIARDLA 187
 DB 118 GKRTYIPAV---KDAAG--GSIVISSAAGLGMALTSYSGASKVGVGSKLAAYELG 171
 QY 188 PGIRMTAPGLFGLPPL--TSLPEKVANFLASQVPPSRG--DPAEYAHLYQAIR-- 242
 DB 172 TIRIRNVSHFPGMTTPMAETGICINQEGNT--PTTPM--GRVGNPGLIAGVYKLLSDT 228
 QY 243 NPLNGEVIRLDG 255
 DB 229 SSYVTGAEALVADG 241
 RESULT 16
 YPFD_BACSU STANDARD; PRT; 255 AA.
 ID YPFD_BACSU STANDARD; PRT; 255 AA.
 AC P39640;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical oxidoreductase ypfD (EC 1.-.-.-).
 GN YPFD OR IPA-82D.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020537; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Mosser I.,
 RA Presseau E., Santana M., Schneider E., Schweizer J., Vertes A.,
 RA Rapoport G., Danchin A.;
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97
 kb region from 325 degrees to 333 degrees";
 RL MOL. Microbiol. 10:371-384(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogatawara N., Mosser I., Albertini A.M., Allion G.,
 RA Azevedo V., Bertorello M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Bortier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.U., Cornerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertlan K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Funa S., Gallizi A., Galleron N.,
 RA Gilm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Guiseppe G., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koelter P., Konigstein G., Krogh S., Kunnano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portetelle D., Portetelle S., Prescott A.M.,
 RA Presseau E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale I.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Solio B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vanier F., Vassarotti A.,
 RA Viari A., Wandut R., Wedler B., Wedler H., Weltenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis";
 RL Nature 390:249-256(1997).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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 CC
 CC EMBL: X73124; CA51638.1; -;
 CC EXBL: 299123; CAB1579.1; -;
 CC PIR: S39737; S39737.
 CC HSSP: P50162; IAE1.
 CC Subtilist; BG10628; ypfD.
 CC InterPro: IPR002198; ADH_short.
 CC Pfam: PF00106; adh_short; 1.
 CC PRINTS: PR00080; SDRFAMILY.
 CC PROSITE: PS00061; ADH_SHORT; 1.
 CC Hypothetical protein; Oxidoreductase; Complete proteome.
 KW NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 FT SEQUENCE 255 AA; 27324 MW; 20AA2259F8B8C9B CRC64;
 Query Match 23.2%; Score 302; DB 1; Length 255;
 Best Local Similarity 32.6%; Pred. No. 2,7e-16;
 Matches 86; Conservative 41; Mismatches 101; Indels 36; Gaps 7;
 QY 14 VITGASGLATPRLVYVGVGASAVLLDIPNSGDAQAKKGNCCVAPADYTSKDVQ 72
 DB 11 LITGASGLGYAQAQAFAGQAAVYVADIDAGQEAQAKKNNDRHVFQDITIDEACQ 70
 QY 73 TALALAKGKRGVAVNCAGIYASVSKTYLKKGGHTLEDFOFVLDVNLGTFENVIR 130
 DB 71 HAVESAVTFEGGLDVLINAGIEIVAPHEHE-----LSDMNVLQVNLGMLMSKHA 124
 QY 131 ----LVAGEMQNEPDGQGVYIINTASVAAFEQGVGAQVSAKSGIVGTLPIARDL 186
 DB 125 LKHLIAG-----KGNITNCVSGGLVAMPDIPAYNASKGVLOLITSMADV 172
 QY 187 APGIRMTAPGLFGLPPL-----LTSPEKVANFLASQVPPSRGDPADYAHLYQ 238
 DB 173 AKHQIRNVAVCPGIDTFLNKSFLNNEGTLIEIKREKAVNPL-LRLGKPEIAYMVL 231

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FT NP_BIND 9 33 NADP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
FT CONFLICT 23 23 D -> A (IN REF. 1).
SQ SEQUENCE 246 AA; 26282 MM; 6A391167D237DC CRC64;

Query Match 23.9%; Score 311.5; DB 1; Length 246;
Best Local Similarity 29.7%; Pred. No. 4.8e-17;
Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;

QY 13 AVITGGASGGLAERLVOGASAVLLDPNSGGEQA-----KKGNNCVFPAADY 65
D 7 AIVGAGRGIGRSTALDLANSGANV--VNSGENEKAEEVDEIKSMRKAIANKADY 63
QY 66 TSEKDVOTATLALAKGFRVDVAVNCAGIYASRTYLNKRGQHTLEDFQRLVDVNLMT 125
D 64 SNPDVQNMKEITLSTFSTIDILVNNAGITRDNLIMMKE-----DEMDDVINILKGV 117
QY 126 FNVIRLYAGEMGQNEPDGGRGVIINTASVAAFEGVGGAASASKGIYGLTPARD 185
D 118 FNCKRAVTRQMKR-----RSGRINVSSTIVGSGNPGQANTYAAAGAYIGLTKSSAK 171
QY 186 LAPGIRVMTAPGLFTPLTSLPERVANFLASQVFPSPRLGDPARYAHLVQAIIEN- 243
D 172 LASNITVYNAIAPFISIDMTDKLAKVDQEMLKQITL-ARFGPSDVSSVVFELASGA 230
QY 244 PFLNGEYVRLDGAIRM 259
D 231 RYMTGQTLHIDGMVM 246

RESULT 14
YK02_MYCTU STANDARD; PRT; 260 AA.
ID YK02_MYCTU
AC Q10855;
DT 01-OCT-1996 (Rel. 34, Created)
DI 15-JUL-1999 (Rel. 38, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase Rv2002 (EC 1.-.-.-).
GN FABG3 OR Rv2002 OR MT2058 OR MTCY39.16C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriia (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Petwell T., Gentles S., Hamlin N., Holroyd S.,
RA Horsby T., Jagsen K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellon S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the Biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Milada A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/Genbank/DBD databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
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CC -----
DR EMBL: 274025; CA98414.1;
DR EMBL: AE007057; AAK46335.1;
DR HSSP: P19992; LHDC.
DR TIGR: MT2058;
DR TIGR: Rv2002;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 11 35
FT ACT_SITE 153 153 NAD (BY SIMILARITY).
FT CONFLICT 174 174 S -> G (IN REF. 2).
SQ SEQUENCE 260 AA; 27030 MM; 0935A14ED36220B7 CRC64;

Query Match 23.4%; Score 305; DB 1; Length 260;
Best Local Similarity 33.9%; Pred. No. 1.6e-16;
Matches 85; Conservative 41; Mismatches 99; Indels 26; Gaps 5;

QY 10 GVAVITGGASGGLAERLVOGASAVLLDPNSGGAQAKKGGNNCVFAPADVTSBK 69
D 7 GKVALVSGARGGASHVRAVNAEAGKAVFGDILDEGVAALADAAARIYHLDVTPA 66
QY 70 DVQATLALAKGKFRVDVAVNCAGIYASRTYLNKRGQHTLEDFQRLVDVNLMTFNYI 129
D 67 QWTAADVTAVTAPAGLHVLNNAGI-----INIGTIEDYALTEMRILDVNLTVGLFI 120
QY 130 RLYAGEMGQNEPDGGRGVIINTASVAAFEGVGGAASASKGIYGLTPARDLAPI 189
D 121 RAVV-----KPKKEKRGSIINISSIEGLAGVACHGTATKFAVAGLTKSTALELGS 174
QY 190 GIRVMTAPGLFTPLTSLPERVANFLASQVFPSPRLG--DPAEYAHV--QAIIENP 244
D 175 GIYVNSHPELVTPMTDWPEDI-----FQALGRAEPVEVSMVLYVLADESS 225
QY 245 FLNGEYVRLDG 255
D 226 YSTGAERFVDG 236

RESULT 15
2BHD_STREX STANDARD; PRT; 255 AA.
ID 2BHD_STREX
AC P19992;
DT 01-FEB-1991 (Rel. 17, Created)
DI 01-FEB-1991 (Rel. 17, Last sequence update)
DR 01-NOV-1997 (Rel. 35, Last annotation update)
DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Actinobacteria; Actinobacteriia (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
[1]
RP SEQUENCE.
RX MEDLINE=90306362; PubMed=2194840;
RA Marekov L., Krok M., Joernvall H.;
RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
RT 'short-chain non-metalloenzyme' alcohol dehydrogenase type."
RL FESB Lett. 266:51-54 (1990).
[2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=92052211; PubMed=1946424;
RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
RA Rimsay R.L., Orr J.C.;
RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
RT dehydrogenase: a member of a short-chain dehydrogenase family."

```


CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NAD(+) = 3-oxoacyl-[acyl-carrier protein] + NADP.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC -----
 CC EMBL: D90907; BAA17614.1; -
 CC HSSP: P50162; 1AEL.
 CC InterPro: IPR002198; ADH_short.
 CC Pfam: PF00106; adh_short; 1.
 CC PRINTS: PRO0080; SDRFAMILY.
 CC PROSITE: PS00061; ADH_SHORT; 1.
 CC Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
 CC NE_BIND 11 35 NADP (BY SIMILARITY).
 CC ACT_SITE 156 156 BY SIMILARITY.
 CC SEQUENCE 247 AA; 25724 MW; 91EBF9409C77F20 CRC64;
 SQ
 Query Match 24.0%; Score 313.5; DB 1; Length 247;
 Best Local Similarity 32.1%; Pred. No. 3,4e-17;
 Matches 85; Conservativity 45; Mismatches 92; Indels 43; Gaps 8;
 QY 12 VAVITGGASGLGATLERVGGG-----ASAYLDLPSSGGEQAQKRGNNC 58
 DB 8 VALVTGASRGIGKATLALATATMKVYVNAOSSTADAVAEITANGGA----- 58
 QY 59 VFAPADVTSKEDVQTALATLAKFKGRVDYAVNCAJAVASKTNLKQGTHTLEDFQRYL 118
 DB 59 IAVQANVANDVDQILKTLDFSRDYLAVNNAAGITRDLILRMK-----LEDMQAVY 112
 QY 119 DVNLMTGFNVIRLVAGMGQNEPDQGGQRCVITNTSVAFPEQVQQAAYSAGKGIYGV 178
 DB 113 DLNLTGVFLCTKAVSKMLMQ-----KSGRIINISVAAQMNPOQANISAKKAGVIGP 166
 QY 179 TLPIARDLAPIGIRVMTIAPGLFGTPLLTL-PEKVANFLASGVPPSRUGDPAEYAHLY 237
 DB 167 TKYVAKELASRGVYVNAVNAFGFLATMDTENLNAEPILGF-----IPL-ARYGQPEYVAGTI 221
 QY 238 QAITENP---FLNGEVIRLDGAIRM 259
 DB 222 RFLATDPAALVITIGTFNVGVGMV 246
 RESULT 13
 FABG_BACSU STANDARD: PRT; 246 AA.
 ID FABG_BACSU
 AC P51831; O31733;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketocacyl-
 DE acyl carrier protein reductase).
 GN FABG.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96326321; PubMed=8759840;
 RA Morbidoni H.R., de Mendoza D., Cronan J.E. Jr.;
 RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
 RT lipid biosynthesis genes."
 RL J. Bacteriol. 178:4794-4800(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Koszer I., Albertini A.M., Aloni G.,
 RA Azevedo V., Berto M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
 RA Deltzer F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabre C., Ferrari E., Follger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grand G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech Y., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapides A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noack M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Serr S.J., Serr P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wamutt R., Wedler E., Wedler H., Wellenreger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunio K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis."
 RT Nature 390:249-256(1997).
 RL [3]
 RN SEQUENCE OF 1-172 FROM N.A.
 RP STRAIN=168;
 RC MEDLINE=98195738; PubMed=9534248;
 RX Foulger D., Errington J.;
 RT "A 28 kbp segment from the spvM region of the Bacillus subtilis 168
 RT genome."
 RL Microbiology 144:801-805(1998).
 RN [4]
 RP SEQUENCE OF 230-246 FROM N.A.
 RC STRAIN=168;
 RX Oguro A., Kakeshita H., Takematsu H., Nakamura K., Yamane K.;
 RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NAD(+) = 3-oxoacyl-[acyl-carrier protein] + NADP.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC -----
 CC EMBL: U59433; AAC44307.1; -
 CC EMBL: Z99112; CAB13464.1; -
 CC DR EMBL: Y13937; CAAT74250.1; -
 CC DR EMBL: D64116; BAA10974.1; -
 CC DR HSSP: Q12634; 1YBV.
 CC Subtilist: Bg11535; fabg.
 CC InterPro: IPR002198; ADH_short.
 CC Pfam: PF00106; adh_short; 1.
 CC PRINTS: PRO0080; SDRFAMILY.
 CC PROSITE: PS00061; ADH_SHORT; FALSE_NEG.
 CC Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
 KM

AC Q92506; Q90101; 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estradiol 17 beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-HSD 8) (17-beta-hydroxysteroid dehydrogenase 8) (Kee protein) (Kee-6).
 GN HSD17B8 OR HKE6 OR RING2 OR FABGL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tubby B.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 3-261 FROM N.A.
 RX MEDLINE=97001166; PubMed=8812499;
 RA Ando A., Kikuchi Y., Shigenari A., Kawata H., Okamoto N., Shima T., Chen L., Ikemura T., Abe K., Kimura M., Inoko H.;
 RT "CDNA cloning of the human homologues of the mouse Kee4 and Kee6 genes at the centromeric end of the human MHC region.";
 RL Genomics 35:600-602(1998).
 CC -1- FUNCTION: USES ESTRADIOL AS ITS PREFERRED SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P)(+) = estrone + NAD(P)H.
 CC -1- PATHWAY: BIOSYNTHESIS OF ESTROGENS.
 CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE LIVER AND PANCREAS, LOWER IN THE SKELETAL MUSCLE AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.
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 CC -----
 DR EMBL: AL031228; CAC38444.1;
 DR EMBL: D82061; BA011529.1;
 DR HSSP: 070351; 1E6W.
 DR GeneW: HGNC:3554; HSD17B8.
 DR MIM: 601417;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KW Steroid biosynthesis; Oxidoreductase; NAD; Multigene family.
 FT NP_BIND 5
 FT ACT_SITE 169
 FT CONFLICT 117
 FT CONFLICT 193
 FT CONFLICT 208
 FT CONFLICT 212
 FT CONFLICT 212
 SQ SEQUENCE 261 AA; 26974 MW; 8BBB2D713171AD71 CR664;
 Query Match 25.6%; Score 333.5; DB 1; Length 261;
 Best Local Similarity 31.2%; Pred. No. 1.1e-18;
 Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
 DB 8 VGLVAVITGASGGLATAEERLVGGASAVLLDLPNSGGEAQAKL-----GN 56
 DB 9 LNSALALVYAGSGGIRAVSVRLAGEGATVACDDRAAAGQTVRLGPGSGKEPPGNGN 68
 DB 57 NCVFAPADVTSEKDVOTALAKKFGFR-VDVAVNCAGIAVASKTYNNKKGOTHTLEDPO 115
 DB 69 HAAF-CADVSEARAACLLLEVOYACPSRPVSVVSCAGITODEFLIHSE-----DWD 121
 DB 116 RYLVAVLMGTFPVNTRLVAGMGONGNEPDGSGGVITNTSVAAFEVGVOGAAYASAKGI 175
 DB 122 KYIAVNLKGTFLVTAQAALVSN-----GCRGSIINISIVGKYGNGVGTATYAAKAGV 176

QY 176 VGMTPLPARDLAPGIRKMTIAPGLFETPLLSPEKVFANFLASQVFFSRIGDPAEYAH 235
 DB 177 IGLTQTARELGRHIGRINCNSVLLPFIATPMTOKVQKVKVEMIPM-CHLGDPEVDAD 235
 QY 236 LYO-ATLENPFLNGEYIRLDGAIRM 259
 DB 236 VVAFPLASEDSGYITGTSVEVTGLFM 261
 RESULT 10
 ID FABG_VIBCH STANDARD; PRT; 244 AA.
 AC Q9K0H7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 GN FABG OR VC2021.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eilen J.A., Nelson W.C., Clayton R.A., Gwin M.L., Dodson R.J., Hatt D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dracoli I., Sellers P., McDonald L., Ueberback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
 RL Nature 406:477-483(2000).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NAD(P)(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SCR) FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE004276; AAF5169.1; ALT_INIT.
 DR HSSP: P19992; 1HDC.
 DR TIGR: VC2021;
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT.1.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 10
 FT ACT_SITE 151
 FT ACT_SITE 151
 SQ SEQUENCE 244 AA; 25566 MW; 9FB28278D7C3CE CRC64;
 Query Match 25.3%; Score 330.5; DB 1; Length 244;
 Best Local Similarity 32.0%; Pred. No. 1.7e-18;
 Matches 82; Conservative 54; Mismatches 103; Indels 17; Gaps 5;
 QY 7 SVKGLVAVITGASGGLATAEERLVGGASAVLLDLPNSGGEAQAKLGNCFAPADVT 66
 DB 2 NLEKVALVYAGSGGIRAVSVRLAGEGATVACDDRAAAGQTVRLGPGSGKEPPGNGN 61
 QY 67 SEKDVOTALAKKFGFRVDVAVNCAGIAVASKTYNNKKGOTHTLEDPOFORYLVNMGTF 126

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of *Thermotoga maritima*.";
 RL Nature 396:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC -----
 DR EMBL: AB001811; AAD36790.1; .
 DR HSSP: P50162; IAEI.
 DR TIGR: TM1724; .
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Fatty acid biosynthesis; Oxidoreductase; NADP: Complete proteome.
 FT NP_BIND 10 34 NADP (BY SIMILARITY).
 FT ACT_SITE 134 154
 FT SEQUENCE 246 AA; 26401 MW; 8C08904D28099142 CRC64;
 SO
 Query Match 26.3%; Score 343; DB 1; Length 246;
 Best Local Similarity 33.7%; Pred. No. 1.9e-19;
 Matches 86; Conservative 47; Mismatches 104; Indels 18; Gaps 5;
 QY 8 VAGLVAVITGASGGLAERLVGGASAVLLDPNSGGA---QAQKLNCFYAAD 64
 DB 3 LKQKVLITGASGIGKATTLTFAQEGATVAGDISKENVSLVKEAGLPEKYPVYN 62
 QY 65 VTSEKDVOTALAKKRGFRVAVAVACAGIAVASKTYNKKQGTLLDFQFVLDVNLNG 124
 DB 63 VYDRDQIKVEVEKYQKGRIDIVNNGITRDALLVRKE-----EDMDAVIVNLKG 116
 QY 125 TENVIRLVAGENGQNEPDGOGGVYINTASYAAVEGQVGAAYASAKSGIYGMTLPAR 184
 DB 117 VFNVTGMVVPYMKQ-----RNGSLVNVSVVGYIGNGQNYAASRAGVIGMTKMAK 170
 QY 185 DLAPIGIRVWTAPGLFGTPLTSLPEKVAANFLASOVPPSRIGDPAEYAHV--QAITE 242
 DB 171 ELAQRIRVNAVAPGIEFTPEKRLPEKARFETALSRIP-GRFGKPEEVAQVILLABDE 229
 QY 243 NPFLNGEVIRLDGAI 257
 DB 230 SSYVTQGVIGIDGGL 244
 RESULT 8
 FABG_CUPLA STANDARD; PRT; 320 AA.
 ID FABG_CUPLA
 AC P28643;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor
 DE (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
 GN CLKR27.
 OS Cuphea lanceolata.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Lythraceae; Cuphea.
 OX NCBI_TaxID=9930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2293104; PubMed=1376402;
 RA Klein B., Pawlowski K., Hoerlcke-Grandpierre C., Schell J.,
 RA Toepfer R.,
 RT "Isolation and characterization of a cDNA from *Cuphea lanceolata*
 RT encoding a beta-ketoacyl-ACP reductase.";
 RL Mol. Gen. Genet. 233:122-128(1992).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
 CC PLASTIDS.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X64566; CAA45866.1; .
 DR PIR: S19832; S19832.
 DR HSSP: P50162; IAEI.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KM Fatty acid biosynthesis; Oxidoreductase; NADP: Chloroplast;
 FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 62 320
 FT NP_BIND 82 106
 FT ACT_SITE 227 227 NADP (BY SIMILARITY).
 FT SEQUENCE 320 AA; 33103 MW; 06BAF0522B28C87 CRC64;
 SO
 Query Match 25.7%; Score 335; DB 1; Length 320;
 Best Local Similarity 32.7%; Pred. No. 1e-18;
 Matches 87; Conservative 46; Mismatches 111; Indels 22; Gaps 6;
 QY 2 AAACRSYKGLVAVITGASGIGLTAERLVGGASAVLLDPNSGGA---QAQKLN 56
 DB 69 AGAQQSVESPVIYTGASRGKALALSL-GKACRYLVAVASSKAEVSEIEFGG 127
 QY 57 NCVPAPADVTESEKDVOTALAKKRGFRVAVAVACAGIAVASKTYNKKQGTLLDFQF 116
 DB 128 QALTFGGVSKSEDEVEAMIKTAVDAKGTVIDVNNAGITDGLMKRKSQ-----WQE 181
 QY 117 VLDVNLNGTENVIRLVAGENGQNEPDGOGGVYINTASYAAVEGQVGAAYASAKSGIY 176
 DB 182 VIDNLGTGVFLCTQAAKIMKK-----KKGRILINIASVVGIVGNGAQNTSAKAGVI 235
 QY 177 GMTLPIDADLAPIGIRVWTAPGLFGTPLTSLPEKVAANFLASOVPPSRIGDPAEYAHV 236
 DB 236 GFTKTVAREYASRNINNAVAPGISDMSKGLDDINKKILLETIP-GRYGOPEEVAAGL 294
 QY 237 VQAILNEP--FLNGEVIRLDGAIM 259
 DB 295 VEFALINPASSYVVGQVFTIDGGM 320
 RESULT 9
 DHB8_HUMAN STANDARD; PRT; 261 AA.
 ID DHB8_HUMAN

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DR EMBL: AE003507; AAF48797.1; -
DR HSSP: O70351; 1E6W
DR FlyBase: FBgn0021765; scu.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR Oxidoreductase; NAD; Mitochondrion.
KW NP_BIND
FT ACET_SITE 6 31 NAD (BY SIMILARITY).
FT MOTIF 162 162 BY SIMILARITY.
FT MOTIF 33 33 L->Q; LETHAL ALLELE.
FT MOTIF 120 120 F->I; LETHAL ALLELE.
SQ SEQUENCE 255 AA; 26905 MW; F58690643FA0FD03 CRC64;

Query Match
Best Local Similarity 69.8%; Score 910; DB 1; Length 255;
Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGLVAVTTGASGIGLTAERLYGQASAVLLDLPNSGGEAQAQKKGNNCVPAPDVTS 67
DB 2 IKNAVSLVTGASGSGRATAEERLAKQASVTLADLPSSKGNVAKELGDKVFEVPDVTS 61
QY 68 EKDVOTALAKGKGRVAVNAGIAVASKTYNLKGGTHTLEDFORVLDVNLKGFEN 127
DB 62 EKDVSAALQTAQKDFGRDLTVNCAQATRAKTENKNAHREDFORVINTVGTEN 121
QY 128 VIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGOVQQAAYASAKSGIVGTLPIARDLA 187
DB 122 VIRLVAGEMQNEPDQGGQGVIIINTASVAAFEGOVQQAAYASAKSGIVGTLPIARDLA 181
QY 168 PLGIVMTIAGLTFETPLLTSLPEKVNFLASQVPEPRIGDPAEYAHVQALIEENPLN 247
DB 162 TGGINICITAPLEPTPLALPEKVRTFLAKSTPEPRIGDPAEYAHVQALIEENPLN 241
QY 248 GEVIRLDGAIKMP 261
DB 242 GEVIRLDGAIKMP 255

RESULT 6
YD50_MTCUTU STANDARD; PRT; 247 AA.
AC Q11020;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase RV1350 (EC 1.-.-.-).
GN FABG2 OR RV1350 OR MT1393 OR MTCY02B10.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA MEDLINE=96295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jorgels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Ruster J.E., Taylor K., Whitehead S., Squares S., Squares R.,
RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

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RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
DR EMBL: Z75555; CAAG9983.1; -
DR EMBL: AE007012; AAK45656.1; -
DR HSSP: O70351; 1E3S.
DR TIGR: MT1393; -
DR Tuberculist; RV1350; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 9 34 NAD (BY SIMILARITY).
FT ACET_SITE 155 155 BY SIMILARITY.
SQ SEQUENCE 247 AA; 25871 MW; 76CA07892E7BB873 CRC64;

Query Match
Best Local Similarity 29.3%; Score 382.5; DB 1; Length 247;
Matches 96; Conservative 43; Mismatches 91; Indels 17; Gaps 5;

QY 13 AVITGASGIGLTAERLYGQASAVLLDLPNSGGEAQAQKKGNN-CVPAPDVTSKD 70
DB 10 AVITGASGIGLTAERLYGQASAVLLDLPNSGGEAQAQKKGNN-CVPAPDVTSKD 69
QY 71 VQPLALAKGKGRVAVNAGIAVASKTYNLKGGTHTLEDFORVLDVNLKGFENVR 130
DB 70 VQPLALAKGKGRVAVNAGIAVASKTYNLKGGTHTLEDFORVLDVNLKGFENVR 123
QY 131 LVAGEMQNEPDQGGQGVIIINTASVAAFEGOVQQAAYASAKSGIVGTLPIARDLA 190
DB 124 LVAGEMQNEPDQGGQGVIIINTASVAAFEGOVQQAAYASAKSGIVGTLPIARDLA 177
QY 191 IRVVTIAPGLEFETPLLTSLPEKVNFLASQVPEPRIGDPAEYAHVQALIEENPLN 248
DB 178 IRVVTIAPGLEFETPLLTSLPEKVNFLASQVPEPRIGDPAEYAHVQALIEENPLN 236
QY 249 EVIRLDG 255
DB 237 EVIRLDG 243

RESULT 7
FABG_THEMEA STANDARD; PRT; 246 AA.
AC Q9X248;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR TM1724.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RA MEDLINE=99287316; PubMed=10360571;

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 CC NCBI_Taxid=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C57BL/6 X GBA.
 CC Fu J., Chen X., Stern D., Yan S.D.;
 CC Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH;
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC -----
 CC EMBL: U96116; AAB57689.1; ALT_INIT.
 CC DR HSSP: C070351; 1E6W.
 CC DR SWISS-2DPAGE: C08756; M0USE.
 CC DR MGD: MG1:133871; Hsd17D10.
 CC DR InterPro: IPR002198; ADH_short.
 CC DR Pfam: PF00106; adh_short.1.
 CC DR PRINTS: PRO0080; SDRFAMILY.
 CC DR PROSITE: PS00061; ADH_SHORT; 1.
 CC KM Oxidoreductase; NAD.
 CC FT NP_BIND 12 37 NAD (BY SIMILARITY).
 CC FT ACT_SITE 168 168 BY SIMILARITY.
 CC SQ SEQUENCE 261 AA; 27418 MW; 61213B13E283D41 CRC64;
 CC
 CC Query Match 87.0%; Score 1134; DR 1; Length 261;
 CC Best Local Similarity 86.2%; Pred. No. 6.3e-80;
 CC Matches 225; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
 CC
 CC QY 1 MAACRSVGLAVITGASGIGLATAEVLVGGASAVLLDPNSGGENAKKIGNCF 60
 CC Db 1 MAAVASVGLAVAVTGGASGPMWAKTAVLVDPDESGEQAKKIGESCIF 60
 CC QY 61 AAPADVTSEKDVATLALAKGRGVAVNCGIAVASTYLLKGGHTLDEPRVVD 120
 CC Db 61 AAPAVTSEKIDAAITLAKERGRIDVAVNCGIAVASTYLLKGGHTLDEPRVVD 120
 CC QY 121 NMGTGTVRLVAGENGNEPDGGRGVITNTASVAFEGGVQAAVSASKGIIVMTL 180
 CC Db 121 NMGTGTVRLVAGENGNEPDGGRGVITNTASVAFEGGVQAAVSASKGIIVMTL 180
 CC QY 181 PIARDLAPGIRVMTAPGLGTPPLTSPKAVANFLAQVPPPSLSPAPYAHVQAI 240
 CC Db 181 PIARDLAPGIRVMTAPGLGTPPLTSPKAVANFLAQVPPPSLSPAPYAHVQAI 240
 CC QY 241 IENPFLNGEYIRLDGAIKMP 261
 CC Db 241 IENPFLNGEYIRLDGAIKMP 261
 CC
 CC RESULT 5
 CC HCD2_DROME STANDARD; PRT; 255 AA.
 CC ID HCD2_DROME
 CC AC 018404;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II NADH)
 CC DE (Scully protein).
 CC GN SCU OR CG7113.
 CC OS Drosophila melanogaster (Fruit fly).
 CC CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_Taxid=7227;
 CC [1]
 CC SEQUENCE FROM N.A. AND MUTAGENESIS OF LEU-33 AND PHE-120.
 CC STRAIN=Canlon S;
 CC MEDLINE=98252852; Pubmed=9585418;
 CC Torroja L., Ortuno-Sanagu D., Ferrus A., Haemmerle B., Barbás J.A.;
 CC "Scully, an essential gene of Drosophila, is homologous to mammalian
 CC mitochondrial type II L-3-hydroxyacyl-CoA dehydrogenase/amyloid beta
 CC peptide-binding protein".
 CC J. Cell Biol. 141:1009-1018(1998).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=Berkley;
 CC MEDLINE=20196006; Pubmed=10731132;
 CC Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 CC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 CC Sutton R.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 CC Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 CC Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
 CC Abrah J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 CC Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 CC Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 CC Borokova D., Botchan M.R., Bouck J., Brinkstein P., Brotler P.,
 CC Butts K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 CC Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 CC de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 CC Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 CC Durbin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,
 CC Fouts C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 CC Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 CC Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 CC Hostalin D., Houston K.A., Howland T.J., Wei M.-H., Ideyama C.,
 CC Jaislin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 CC Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 CC Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 CC Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 CC Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 CC Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 CC Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 CC Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 CC Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 CC Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 CC Spier E., Spredlin A.C., Stapleton M., Strong R., Sun E.,
 CC Switz R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 CC Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 CC Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 CC Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou G., Zhao Q., Zheng L.,
 CC Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 CC Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 CC "The genome sequence of Drosophila melanogaster".
 CC Science 287:2185-2195(2000).
 CC -1- FUNCTION: MAY PLAY A ROLE IN GERM LINE FORMATION.
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
 CC + NADH.
 CC -1- SUBUNIT: MULTIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- TISSUE SPECIFICITY: FOUND IN MANY TISSUES INCLUDING CNS. HIGHEST
 CC EXPRESSION IN BOTH EMBRYONIC GONADAL PRIMORDIA AND MATURE OVARIES
 CC AND TESTES.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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 CC EMBL: Y15102; CAA75377.1; .

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CC EMBL; AB002156; BAA19510.1; -

DR HSSP; 070351; 1E6W.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short.1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT.1.

KW Oxidoreductase; NAD; Mitochondrion.

FT NP_BIND 12 37 NAD (By SIMILARITY).

FT ACT_SITE 168 168 BY SIMILARITY.

FT SEQUENCE 261 AA; 27140 MW; 8C7572B6A9A49780 CRC64;

Query Match 92.6%; Score 1208; DB 1; Length 261;

Best Local Similarity 92.0%; Pred. No. 1,4e-85;

Matches 240; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAACRSVGLVAVITGASGLATAEELVVGASAVLLDLPNSGGEAAKKLGNNCF 60

DB 1 MAACRSVGLVAVITGASGLATAEELVVGASAVLLDLPNSGGEAAKKLGSCAF 60

QY 61 APADVTSEKDVQALALAKGKRGVDVAVNCAGIYASTYLNKKQHTLDFQVIVN 120

DB 61 APADVTSEKDVQALALAKGKRGVDVAVNCAGIYASTYLNKKQHTLDFQVIVN 120

QY 121 NMGTENVIRLVAGENGQNEPDGQGVYINTASVAEEGVGQAAVSASKGIYGMTL 180

DB 121 NMGTENVIRLVAGENGQNEPDGQGVYINTASVAEEGVGQAAVSASKGIYGMTL 180

QY 181 PIARDIAPGIRVMTAPGLFGTPLLSTPEKYANFLASQVPPPSLGPAYAHLYQAI 240

DB 181 PIARDIAPGIRVMTAPGLFGTPLLSTPEKYANFLASQVPPPSLGPAYAHLYQAI 240

QY 241 IENPFLNGEYIRLDGAIKMP 261

DB 241 IENPFLNGEYIRLDGAIKMP 261

RESULT 3

HCD2_RAT STANDARD; PRT; 260 AA.

AC 070351: 090YD4:

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR ERAB.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Gunn-Moore F.J., Tavaire J.M.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RA Yang S.-Y., He X.-Y.;

RL "Molecular cloning and characterization of the cDNA of rat brain short chain L-3-hydroxyacyl-CoA dehydrogenase."

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RC TISSUE=Brain;

RA MEDLINE=20481418; PubMed=11023795;

RA Powell A.J., Read J.A., Banfield M.J., Gunn-Moore F., Yan S.D., Lustbader J., Stern A.R., Stern D.M., Brady R.L.;

"Recognition of structurally diverse substrates by type II 3-hydroxyacyl-CoA dehydrogenase (HADH II)/amyloid-beta binding alcohol dehydrogenase (ABAD)."

RL J. Mol. Biol. 303:311-327(2000).

CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

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CC EMBL; AF049878; AAC05747.1; -

DR EMBL; AF069770; AAF14853.1; -

DR PDB; 1E3W; 25-MAY-01.

DR PDB; 1E3S; 25-MAY-01.

DR PDB; 1E6W; 25-MAY-01.

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short.1.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH_SHORT.1.

KW Oxidoreductase; NAD; Acetylation; 3D-structure.

FT INIT_MET 0 0

FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).

FT NP_BIND 11 35 NAD (BY SIMILARITY).

FT ACT_SITE 167 167 BY SIMILARITY.

FT CONFLICT 4 4 V->C (IN REF. 2).

FT SEQUENCE 260 AA; 27114 MW; 30F7E723A95F9227 CRC64;

Query Match 88.4%; Score 1153; DB 1; Length 260;

Best Local Similarity 87.7%; Pred. No. 2.2e-81;

Matches 228; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 2 AAACRSVGLVAVITGASGLATAEELVVGASAVLLDLPNSGGEAAKKLGNNCF 61

DB 1 AAACRSVGLVAVITGASGLATAEELVVGASAVLLDLPNSGGEAAKKLGNNCF 60

QY 62 PADVTSEKDVQALALAKGKRGVDVAVNCAGIYASTYLNKKQHTLDFQVIVN 121

DB 62 PADVTSEKDVQALALAKGKRGVDVAVNCAGIYASTYLNKKQHTLDFQVIVN 120

QY 122 LMGTENVIRLVAGENGQNEPDGQGVYINTASVAEEGVGQAAVSASKGIYGMTL 181

DB 122 LMGTENVIRLVAGENGQNEPDGQGVYINTASVAEEGVGQAAVSASKGIYGMTL 180

QY 182 IARDIAPGIRVMTAPGLFGTPLLSTPEKYANFLASQVPPPSLGPAYAHLYQAI 241

DB 182 IARDIAPGIRVMTAPGLFGTPLLSTPEKYANFLASQVPPPSLGPAYAHLYQAI 240

QY 242 ENPFLNGEYIRLDGAIKMP 261

DB 242 ENPFLNGEYIRLDGAIKMP 260

RESULT 4

HCD2_MOUSE STANDARD; PRT; 261 AA.

AC 008756;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)

DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein).

GN HADH2 OR HSD17B10 OR ERAB.

OS Mus musculus (mouse).

HC02_HUMAN
ID HC02_HUMAN STANDARD: PRT: 261 AA.
AC 099714;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
DE (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) (short-chain type dehydrogenase/reductase XH86G2).
GN HADH2 OR ERAB OR XH9G2 OR SCHAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_Taxid=9606;
OX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97478528; PubMed=9338779;
RA Yan S.D., Fu J., Soto C., Chen X., Zhu H., Al-Mohanna F., Collins K., Zhu A., Stern E., Saldo T., Tohyama M., Ogawa S., Rober A., Stern D.;
RA "An intracellular protein that binds amyloid-beta peptide and mediates neurotoxicity in Alzheimer's disease.",
RT Nature 389:689-695(1997).
RL [2]
RN SEQUENCE FROM N.A.
RA Zhuchenko O.P., Wehnert M., Bailey J., Sun Z.S., Lee C.C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE=98337980; PubMed=9671743;
RA Miller A.P., Willard H.F.;
RT "Chromosomal basis of X chromosome inactivation: Identification of a multigene domain in Xp11.21-p11.22 that escapes X inactivation.",
RL Proc. Natl. Acad. Sci. U.S.A. 95:8709-8714(1998).
RN [4]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98221216; PubMed=9553139;
RA He X.Y., Schultz H., Yang S.Y.;
RT "A human brain L-3-hydroxyacyl-coenzyme A dehydrogenase is identical to an amyloid beta-peptide-binding protein involved in Alzheimer's disease.",
RL J. Biol. Chem. 273:10741-10746(1998).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS INTRACELLULAR AMYLOID-BETA. BY INTERACTING WITH AMYLOID-BETA, IT MAY CONTRIBUTE TO THE NEURONAL DYSFUNCTION ASSOCIATED WITH ALZHEIMER DISEASE.
CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NORMAL TISSUES BUT IS OVEREXPRESSED IN NEURONS AFFECTED IN AD.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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CC
CC EMBL: U96132; AAC51812.1; -
CC EMBL: U73514; AAB68938.1; -
CC EMBL: AF069134; AAC39900.1; -
CC EMBL: AF035555; AAC15902.1; -
CC EMBL: AF037438; AAC16419.1; -
CC

DR EMBL: BC000372; AAH00372.1; -
DR HSSP: 070351; 1E3S.
DR Genew: HGNC:4800; HADH2.
DR MIM: 300256; -
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; 37
FT NP_BIND 12 37 NAD (BY SIMILARITY).
FT ACT_SITE 168 168 BY SIMILARITY.
SQ SEQUENCE 261 AA; 26923 MW; 9E74F242E3B6FEF1 CRC64;
Query Match 99.7%; Score 1300; DB 1; Length 261;
Best Local Similarity 99.6%; Pred. No. 1.3e-92;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAACRSYKGLVAVITGASGLATPERLYGGASVLLDLPNSGGEAAKTLGNVCF 60
DB 1 MAACRSYKGLVAVITGASGLATPERLYGGASVLLDLPNSGGEAAKTLGNVCF 60
QY 61 APADVTSEKDVQATLALAKGFGVDVAVNACGIAVASKTYNLKGGTHTLEDFORVLDV 120
DB 61 APADVTSEKDVQATLALAKGFGVDVAVNACGIAVASKTYNLKGGTHTLEDFORVLDV 120
QY 121 NLMGTENVIRLVAGEMGONEPDGCGRGVLIINTASVAFEGVQQAAYSASKGIYGMTL 180
DB 121 NLMGTENVIRLVAGEMGONEPDGCGRGVLIINTASVAFEGVQQAAYSASKGIYGMTL 180
QY 121 NLMGTENVIRLVAGEMGONEPDGCGRGVLIINTASVAFEGVQQAAYSASKGIYGMTL 180
DB 121 NLMGTENVIRLVAGEMGONEPDGCGRGVLIINTASVAFEGVQQAAYSASKGIYGMTL 180
QY 181 PIARDIAPIGIRVWTIAPGLEGTPLTSLPEKVNFTASOVPEPSRLGDPAEFAHLYQAI 240
DB 181 PIARDIAPIGIRVWTIAPGLEGTPLTSLPEKVNFTASOVPEPSRLGDPAEFAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIRMQP 261
DB 241 IENPFLNGEVIRLDGAIRMQP 261
RESULT 2
HC02_BOVIN
ID HC02_BOVIN STANDARD: PRT: 261 AA.
AC 002691;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
OX [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=97214648; PubMed=9061028;
RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;
RT "Cloning and expression of cDNA for a newly identified isozyme of bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into mitochondria.",
RL Biochim. Biophys. Acta 1350:317-324(1997).
CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA + NADH.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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Thu Jun 26 06:55:05 2003

us-09-931-186-20.rsp

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:47 ; Search time 7.83333 Seconds

(without alignments) 1381.956 Million cell updates/sec

Title: US-09-931-186-20

Sequence: 1 MAAACRSYKGLAVITGAS.....ENFLNGEVIRLDGAIKMQP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1300	99.7	261	1	HCD2_HUMAN
2	1208	92.6	261	1	HCD2_BOVIN
3	1153	87.4	260	1	HCD2_RAT
4	1134	87.0	261	1	HCD2_MOUSE
5	910	69.8	255	1	HCD2_PROME
6	382.5	29.3	247	1	YD50_MYCTU
7	343	26.3	246	1	FABG_THEMA
8	335	25.7	320	1	FABG_CUPLA
9	333.5	25.6	261	1	DHBB_HUMAN
10	330.5	25.3	244	1	FABG_VIBCH
11	315.5	24.2	260	1	DHBB_MOUSE
12	313.5	24.0	247	1	FAGI_SYNY3
13	311.5	23.9	246	1	FABG_BACSU
14	305	23.4	260	1	YK02_MYCTU
15	302	23.2	235	1	2BHD_STREX
16	296.5	22.7	548	1	Y4V1_RHISN
17	293.5	22.5	244	1	FABG_VIBHN
18	292.5	22.4	248	1	FABG_AOUAE
19	292.5	22.4	249	1	BA71_EUBSP
20	292	22.4	244	1	FABG_ECOLI
21	291.5	22.4	244	1	FABG_ECOLI
22	288	22.1	263	1	UCPA_SALTY
23	287.5	22.0	246	1	PHBB_ALCEU
24	286	21.9	248	1	PHAB_ACISP
25	285.5	21.9	244	1	FABG_SALTY
26	284.5	21.8	256	1	Y019_THEMA
27	283.5	21.7	246	1	NODG_ACOBR
28	282	21.6	259	1	CMPE_PSEPU
29	281.5	21.6	248	1	FABG_CHLNU
30	281	21.5	250	1	LINC_PSEPA
31	279.5	21.4	241	1	PHBB_ZOORA
32	278.5	21.4	289	1	YHDF_BACSU
33	277	21.2	246	1	PHBB_CHRVI

RESULT 1

ALIGNMENTS

DT 01-JUN-2002 (FIREBASEL. 21, last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase.
GN FABG OR ALR1894.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_Taxid=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL, AP003587; BAB73593.1; "
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR01092; HLH_basic.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 26218 MW; 57D0712F8EA6B698 CRC64;

Query Match 25.7%; Score 334.5; DB 16; Length 251;
Best Local Similarity 33.1%; Pred. No. 1.4e-15;
Matches 91; Conservative 46; Mismatches 97; Indels 41; Gaps 7;

QY 1 MAACRSYKGLAVITGASGLGATAEELVGGASA-----VLDLPNSGG 47
DB 1 MAILSENLRGQAVAVTGASRGIGRAIALELANYGATVVVNYASSSTADEVVAEITGAGG 60
QY 48 EAOAKKLGNNCFAPADVTSEKDVOTALALAKGKFGRYDVAVNCAGITAVASKTYNLKKGQ 107
DB 61 EAVALK-----ADVSQVEQVDNLINGAIDKFRIDILVNNAGITRDITLLRMKP-- 109
QY 108 THTLEDFOFVLVDNIMGTFNVIRLVAGEMQNEPDQGRGVIIINTASVAAFEQVQGOA 167
DB 110 ---EDMOAVIDLNTGVLCITRAVSKMLKQ-----RSGRIINITSVAGOMGNPGQAN 159
QY 168 YSASKGIVGMLTPIARDLPIGIRVMTIAPLGSTPLITSLPEKVANFLASOVFPSPRL 227
DB 160 YSAKAGVIGFTKYAKELASRGITVNAVAPGFTATDNTSNLK---SEGILQYIPL-GRY 215
QY 228 GDPAEYAHLYQAIENP---FLNGEVIRLDGAIRM 259
DB 216 GQPEIAGVRFRLADPAAAVYITGQVFNVDDGMV 250

Search completed: June 23, 2003, 14:32:48
Job time : 32.6667 secs

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QY 128 VIRLVAGMGONEDDGGQGVIIINTASVAAEFGVQGAAYASAKGIVGTLPIANDLA 187
DB 121 VIKFASKYMIKK-----RKGIINISSVGLMGVQGANVAASAGIITGKSVAKELA 174
QY 188 PIGIVMTIAPGLFETPLTSLPEKVANFLASOVFPFRLDPAEYAHVVO--AIENPF 245
DB 175 SRGIVVANAAPROFITDITDNTVNLKEDIKAMKSIPL-KRAKPEVEAEVAFLLASASDY 233
QY 246 INGEVIRLDGAI RM 259
DB 234 ITGVIVNDGGMV 247

RESULT 23
QY 09KA03 PRELIMINARY: PRT; 246 AA.
ID 09KA03:
AC 01-OCT-2000 (TREMblrel. 15, Created)
DI 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100).
GN FABG OR BH491.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_Taxid=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125/JCM 9153;
RX MEDLINE=20512582; PUBMED=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirata C., Nakamura Y., Ogasawara N., Kihara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AP001515; BAB06210.1; -.
DR HSSP: P19992; 1HDC.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; UNKNOW.N.1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 246 AA; 26126 MW; 852B95EB8DE9E90 CRC64;

Query Match 25.7%; Score 335.5; DB 16; Length 246;
Best local Similarity 34.2%; Pred. No. 1.2e-15;
Matches 90; Conservative 42; Mismatches 102; Indels 29; Gaps 7;

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RESULT 24
QY 042774 PRELIMINARY: PRT; 297 AA.
ID 042774:
AC 042774:
DI 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 3-oxoacyl-[acyl-carrier protein]-reductase.
GN OAR-1 OR B2A19.180.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_Taxid=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Burger F., Brois B., Weiss H.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte U., Altm V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AF042860; AAB99799.1; -.
DR EMBL: AL380092; CAB98248.1; -.
DR HSSP: O70351; 1B6W.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 297 AA; 31342 MW; 8DC08FEDF584196F CRC64;

Query Match 25.7%; Score 335.5; DB 3; Length 297;
Best local Similarity 31.7%; Pred. No. 1.5e-15;
Matches 97; Conservative 39; Mismatches 103; Indels 67; Gaps 8;

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RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PAOI;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Ertvin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.D., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garner R.L., Goltzer L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RA "Complete genome sequence of *Pseudomonas aeruginosa* PAOI, an
 RT opportunistic pathogen";
 RL Nat 406:959-964(2000).
 CC -1 SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 CC EMBL: AE004854; ANG07777.1; -
 DR HSSP: PS0163; 2AEI.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001064; Crystalin.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR Oxidoreductase; Complete proteome.
 KW SEQUENCE 252 AA; 26720 MW; F1F445AB82C2D8DE CRC64;
 SO
 Query Match 27.2%; Score 355; DB 16; Length 252;
 Best Local Similarity 35.18; Pred. No. 5.7e-17;
 Matches 94; Conservative 40; Mismatches 100; Indels 34; Gaps 7;
 QY 8 VKGLVAVITGASGLGATAEERLVGGASAVLLDLPN-----SGGEAQAQKIG 55
 DB 3 LKDKVILITGGCGGGRAMGEYLAGARLALVDINREERLDEAVAACKAAGDARA---- 58
 QY 56 NNCVFAPADYTSKEDVQTALALAKGFGVADVAVNCAGIAVASKYINLKKQTH--TLED 113
 DB 59 ----YVCNVADDEQVTHVAQVADFGAINGLVNNAIGLRDLGITKVDGSLSKSLAQ 113
 QY 114 FQRLVDVNLMTGFENVTIRLVAGEMGQ--NEPDGGGGRGVIIINTASVAPEGOVQAAYSAS 171
 DB 114 MOSIVDNLGVLCRREVAAKMIELKNE-----GALVNSSISR-AGNNGQAYSAA 165
 QY 172 KGSIVGNTLPIADLAPITGRVTTIPGLFGFPLTSLPEKYANFLASQVPPSRGDA 231
 DB 166 KAGVADDTVMMAKELARKYIRVAGVAPGLETEMTAGMPEALEKKTAGIPL-KRGKRV 224
 QY 232 EYAHVQATENPFLNGEVRILDAIRM 259
 DB 225 EIAHSAVIFENDYYIGRVLELDGRL 252
 RESULT 21
 Q97DA6 PRELIMINARY; PRT; 249 AA.
 ID Q97DA6;
 AC Q97DA6;
 DT 01-OCF-2001 (TREMblrel. 18, Created)
 DT 01-OCF-2001 (TREMblrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE 3-ketocyl-acyl carrier protein reductase.
 GN CAC3574.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_Taxid=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hilti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.,
 RA "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium *Clostridium acetobutylicum*";
 RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL: AE007854; AAK81497.1; -
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 SO SEQUENCE 249 AA; 26247 MW; B13D7EDAC21A626A CRC64;
 Query Match 26.5%; Score 345.5; DB 16; Length 249;
 Best Local Similarity 33.28; Pred. No. 2.5e-16;
 Matches 86; Conservative 56; Mismatches 96; Indels 21; Gaps 6;
 QY 8 VKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQ-----AKKIGNCVFAP 62
 DB 5 LSGVAVVVTGAGRGDGRAIALKLAEGANLV-VNYSSEAEETQRLKEIELELSKAAVAK 63
 QY 63 ADVTSKEDVQTALALAKGFGVADVAVNCAGIAVASKYINLKKQTHLEDFFQRLVDVNL 122
 DB 64 ADISKYDAETIKKALDEGTVIDLVNNGITKDNLLMKKE-----EDPSVINVTN 117
 QY 123 MGFENVIRLVAGEMGQNEPDGGGRVVIINTASVAPEGOVQAAYSASKGIYGMTLPI 182
 DB 118 KGAFNCIKHTSRVLMK-----KSGKTIINISSVIGLGNAGQVNVAAAKAGIIGMTKSV 171
 QY 183 ARDLAPIGIRMTAPIGLFGFPLTSLPEKYANFLASQVPPSRGDAEYAHVQATIE 242
 DB 172 AKELASRITVNAAPGIIKSDMTDLTKORRESIVAAVPL-NKVGAEADVANIYVFLAS 230
 QY 243 --NPFNGEVRILDAIRM 259
 DB 231 DLSVITGQVINVDDGMV 249
 RESULT 22
 Q989W0 PRELIMINARY; PRT; 247 AA.
 ID Q989W0;
 AC Q989W0;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Dehydrogenases with different specificities (related to short-chain
 DE alcohol dehydrogenases).
 GN FABG3 OR TTE1472.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_Taxid=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MR4 / JCM11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.,
 RA "A complete sequence of *T. tengcongensis* genome";
 RL Genome Res. 12:688-700(2002).
 DR EMBL: AE013105; AAM24694.1; -
 KW Complete proteome.
 SO SEQUENCE 247 AA; 26606 MW; 357D82B8C60E7947 CRC64;
 Query Match 26.0%; Score 339.5; DB 16; Length 247;
 Best Local Similarity 34.3%; Pred. No. 6.4e-16;
 Matches 87; Conservative 48; Mismatches 100; Indels 19; Gaps 6;
 QY 12 VAVITGASGLGATAEERLVGGASAVLLDLPN--SGGEA--QAKKIGNCVFAPADYTS 67
 DB 7 VAEVVGSGGICRAVRAVLAARKGFIATYYVDKSAEEVVEVYKHVDALAKCDVSK 66
 QY 68 EXDVQATALAKGFGVADVAVNCAGIAVASKYINLKKQTHLEDFFQRLVDVNLMTGFN 127
 DB 67 YHEVEVAKEVIEEGSIDVYVNNAGITKDNILLKME-----BEMQVIDVNLKGAFN 120

ID	Q99YD6	PRELIMINARY:	PRT	244 AA.			
Db	8	AVITGKXXRRKAGRGAPRRPRL---	ARSAFLPDINDDKGAAVAAGLADKARFENYNS	63			
QY	67	SEKDVTQALALAKGFEGRVYAVNACGILNASKTYNKKQGTHTLEDFQRLVDNVLGTF		126			
Db	64	DEAAVTAIDQADHDELGLNVAACAGILGGRV--	LGRKGPMLAGOGTVNVLGVSF	121			
QY	127	NVIRLVAGEGONGEPDGGQKGVYIINNTASVAAFEGOVGOAAYSASKSGIVGMLTPIARDL		186			
Db	122	NVAKAAANRQOHNEAGTGGERGVIINTASIAAYEGQIGOAAYASKSGVSMTPMAREL		181			
QY	187	APGIRVMTAPGFGTPTLSLPEKY	213				
Db	182	SREGIRVMTAPGFGTPTMDGMEAY	208				
RESULT 18							
Q8XLH1	08XLH1	PRELIMINARY:	PRT:	246 AA.			
AC	08XLH1						
DT	01-MAR-2002 (TReMBLrel. 20, Created)						
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)						
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)						
DE	3-oxoacyl-[acyl-carrier-protein] reductase.						
GN	FABG OR CPEI070.						
OS	Clostridium perfringens.						
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;						
OC	Clostridiales; Clostridaceae; Clostridium.						
CX	NCBI_TaxID=1502;						
RA	SEQUENCE FROM N.A.						
RP	STRAIN=13 / TYPE A;						
RC	Pubmed=11792842;						
RX	Shimizu T., Ohtani K., Hiraoka H., Ohshima K., Yamashita A.,						
RA	Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;						
RL	"Complete genome sequence of Clostridium perfringens, an anaerobic						
RT	flesh-eater";						
RL	Proc. Natl. Acad. Sci. U.S.A. 99:1996-1001(2002).						
DR	EMBL, AP003189; BAB80776.1;-						
DR	InterPro: IPR002198; ADH_short.						
DR	Pfam: PF00106; adh_short; 1.						
DR	PRINTS: PRO0080; SDRFAMILY.						
DR	PROSITE: PS00061; ADH_SHORT; 1.						
KW	Complete proteome.						
SO	SEQUENCE 246 AA; 26267 MW; CD90B8C650ECC817 CRC64;						
Query Match 28.8%; Score 375.5; DB 16; Length 246;							
Best Local Similarity 35.8%; Pred. No. 21e-18;							
Matches 93; Conservative 47; MisMatches 97; Indels 23; Gaps 7							
QY	8	VKGIVAVTTGGASGIGLTAETRLVGOGASAVLLDLPNSGGEAOAKKL-----GNNCVAP	62				
Db	2	LKDKAIVTGGGRIGRAILALKLIDQGAN-IYINRNSDKKEELKALIEKGVATLVK	60				
QY	63	ADVISEKIVQALALAKGFEGRVYAVNACGILNASKTYNKKQGTHTLEDFQRLVDNL	122				
Db	61	CDISFEEDSKNLMDCKEYFGKIDILLVNNAGITKDTLLRMKE-----EDFDNVIDNL	114				
QY	123	MGEFNVILVAGEGONGEPDGGQKGVYIINNTASVAAFEGOVGOAAYSASKSGIVGMLT	181				
Db	115	KGTFCAMKASHASIMLK-----QRFKTIINNTSVYAGNAGOVNYSASKAGVIGLTRS	167				
QY	182	IARDLAPGIRVMTAPGFGTPTLSLPEKYANLDSVPPPSLGDPAEFAHLYQAL	241				
Db	168	LAKELGSGRTIYNAAPGFGTPTMDGMEAY	226				
QY	242	ENP--FLNGEVIRLIDGAIRM	259				
Db	227	SDAANYITGVINVDGMYM	246				
RESULT 19							
ID	Q99YD6	PRELIMINARY:	PRT	244 AA.			

039YD6: 01-JUN-2001 (TREMblrel, 17, Created)
DT 01-JUN-2001 (TREMblrel, 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel, 21, Last annotation update)
DE Putative beta-ketoacyl-ACP reductase (EC 1.1.1.100).
GN FABG OR SPY1749.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Pirretti U.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Seate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian X., Clifton S.W., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan Y., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL: AE006603; AAC3493.1; -
DR HSSP; P50162; IAB1.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR01608; BACINVASINC.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
RW Oxidoreductase; Complete proteome.
SQ SEQUENCE 244 AA; 26002 MW; 67ECE23870D40D65 CRC64;
Query Match 27.4%; Score 357.5; DB 16; Length 244;
Best Local Similarity 35.4%; Pred. No. 3.7e-17;
Matches 92; Conservative 41; Mismatches 102; Indels 25; Gaps 5;
QY 8 VKGLAVITGSGSIGLTAERLVGGASAVLLDLPNSGGEQAQKL-----GNQVF 60
DB 3 IKGNKIFITGTRIGGLMAHQFASLENIYV-----NGRSKISSELYASFTDGVYVT 57
QY 61 APADYTSERKDQVOTALAKKRGFRVDVAVNCAGIYASKITYLNKKQGTHTLEDFQGVLDY 120
DB 58 ISGDVSEASEAKRMVNEAIESIGSDIVLVNNGIT-----NDKLMKLTEDDFERYLKI 111
QY 121 NLMGFFNYRLVAGMGQNEPDGQGVITNTASVAFEGQVGQAASAGGIVGML 180
DB 112 NLTGAFNNTQSLV-----KPIKAKQGIIVSSVGLTGITGQAGANYAASAGKIGFTK 165
QY 181 PIARLAEIGIRVMTIAPLEGTPLTSLPERKVFANLASQVFPSPRLDPAEYAHVQAI 240
DB 166 SVAREVAARNICVNATAPGFIESDVTGLPERMQQIISQIPM-KRIGAKQEVAAHLASF 224
QY 241 IENPLNGEVTPLDGAIRMQ 260
DB 225 VEQDITQGVATIDGKMTWQ 244
RESULT 20
09HW15
ID PRELIMINARY; PRT: 252 AA.
AC 09HW15:
DT 01-MAR-2001 (TREMblrel, 16, Created)
DT 01-MAR-2001 (TREMblrel, 16, Last sequence update)
DT 01-MAR-2002 (TREMblrel, 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA4389.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
NCBI_TaxID=287;
RN [1]

ID Q87217 PRELIMINARY; PRT; 264 AA.
 AC Q87217;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase type II.
 OS Dictyostellium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostellium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and Analysis of Chromosome 2 of Dictyostellium";
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AC115594; AAL92306.1;
 SO SEQUENCE 264 AA; 28795 MW; 3C0007DA1309F294 CRC64;
 Query Match 46.3%; Score 603.5; DB 5; Length 264;
 Best Local Similarity 48.8%; Pred. No. 5,1e-34;
 Matches 127; Conservative 46; Mismatches 78; Indels 9; Gaps 5;
 QY 8 VAGIVAVITGASGLGATAEERLVGASAVLLDLPNSGGEAAKLGNN-CVEAPADVT 66
 DB 3 INKTFVTGASGLGATAEERLVGASAVLLDLPNSGGEAAKLGNN-CVEAPADVT 62
 QY 67 SERDVTALALAKKGRVDVAVNCAGIVASKTYNKKGQHTIEDFORVLDVNLGTF 126
 DB 63 LEDSVTLSEHCLKKEKEIHGVINCAGVAAQVRVK-RDGQVHPDLFTFRVVMNLIGTF 121
 QY 127 NVIRLVAGEM-GONEPD--QG--ORGVINTASVAFEGVGQAAYASAKSGIVGNT 179
 DB 122 NVIRLVADIIHNGNOSKSDGDEBEKEGVFIMTASVAFEGVGQAAYASAKSGIVGNT 181
 QY 180 LPIARLAPIGRVMTIAPGLTGLTSLPERKANFLASQVPPFSRLGDPREYAHVQA 239
 DB 182 LPMARFAPLAKIRINTIAPGTETPEVEMLPQAIKINSIPFSRMKPREFAFLQCH 241
 QY 240 IIEPNLNGEVIRLDGAIRM 259
 DB 242 LIENYINGEVIRLDGARL 261
 RESULT 16
 Q9ABU6 PRELIMINARY; PRT; 260 AA.
 ID Q9ABU6;
 AC Q9ABU6;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE 3-hydroxyacyl-CoA dehydrogenase.
 GN CC0124.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Niernan W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Pladdek N.D., Ely B.,
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Osterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.

DR EMBL; AE005687; AAK22111.1; -
 DR HSSP; 070351; IE35.
 DR TIGR; CC0124; -
 DR InterPro; IPR002198; ADH_short.
 DR InterPro; IPR000205; NAD_binding.
 DR Pfam; PF00106; adh_short.1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT.1.
 DR Oxidoreductase; Complete proteome.
 SO SEQUENCE 260 AA; 27075 MW; 7DC145D069C89029 CRC64;
 Query Match 45.8%; Score 597; DB 16; Length 260;
 Best Local Similarity 51.0%; Pred. No. 1.4e-33;
 Matches 130; Conservative 30; Mismatches 89; Indels 6; Gaps 2;
 QY 11 LVAVITGASGLGATAEERLVGASAVLLDLPNSGGEAAKLGNNCFAPADVTSEKD 70
 DB 7 VAAVITGASGLGATAEERLVGASAVLLDLPNSGGEAAKLGNNCFAPADVTSEKD 64
 QY 71 VQTALALAKKGRVDVAVNCAGIVASKTYNKKGQHTIEDFORVLDVNLGTF 126
 DB 65 VDAFEPKRAAHGQERILVNCAGTGNAPKASNDKAGETKHPDLAFDRIINLVGTF 124
 QY 127 NVIRLVAGEMGONEPDGQGVITNTASVAFEGVGQAAYASAKSGIVGNTLPARDI 186
 DB 125 RCIAKSAKGMIDLEPLDGERGALVNTASVAFEGVGQAAYASAKSGIVGNTLPARDI 184
 QY 187 APIGRVMTIAPGLTGLTSLPERKANFLASQVPPFSRLGDPREYAHVQAIIENPFL 246
 DB 185 MGEGIRVNTIIPGLTNTPLNNAPFAVKAAGLASVPPKRLGHPREYAHVQAIIENPFL 244
 QY 247 NGEVIRLDGAIRMOP 261
 DB 245 NGEVIRLDGGRMAP 259
 RESULT 17
 Q93SJ3 PRELIMINARY; PRT; 443 AA.
 ID Q93SJ3;
 AC Q93SJ3;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE USCS-2p.
 OS Myxococcus xanthus.
 OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 OC Myxococcales; Cytophasterineae; Myxococcaceae; Myxococcus.
 OX NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CECT 422;
 RA Poza M., Sileiro C., Villa T.G.;
 RT "Clone USCS from Myxococcus xanthus CECT 422 strain";
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL; AY033405; AAK49009.1; -
 DR InterPro; IPR002198; ADH_short.
 DR InterPro; IPR001092; HLM_basic.
 DR Pfam; PF00106; adh_short.1.
 DR Pfam; PF01132; EFP.1.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 SO Oxidoreductase.
 SEQUENCE 443 AA; 47589 MW; 214157E0D55FA20 CRC64;
 Query Match 29.6%; Score 386; DB 2; Length 443;
 Best Local Similarity 46.4%; Pred. No. 8.2e-13;
 Matches 96; Conservative 29; Mismatches 70; Indels 12; Gaps 5;
 QY 13 AVITGASGLGATAEERLVGASAVLLDLPNSGGEAAKLGNNCFAPADVT 66
 DB 11 VAVITGASGLGATAEERLVGASAVLLDLPNSGGEAAKLGNNCFAPADVT 62

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Db      187 MTIAPGIFETPMAGTETEVRSALAGVPFPPRLGRPOEYALAHNIENSMNGEVIRL 246
Qy      254 DGAIRM 259
        |||:|
Db      247 DGAIRM 252

RESULT 13
ID      08UR12      PRELIMINARY;      PRT;      257 AA.
AC      08UR12;
DT      01-JUN-2002 (TREMBlrel. 21, Created)
DT      01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      3-hydroxyacyl-CoA dehydrogenase type II.
GN      ATU1415 OR AGR_C.2613.
OS      Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OX      Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE-21608550; PubMed-11743193;
RA      Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA      Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA      Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,
RA      Chapman P., Clendenning J., Deatherage G., Gillet M., Grant C.,
RA      Kutyavin T., Levy R., Li M.-J., McCelland E., Palmeri A.,
RA      Raymond C., Rose G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA      Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA      Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA      Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA      Nester E.W.;
RT      The genome of the natural genetic engineer Agrobacterium tumefaciens
RT      C58.
RL      Science 294:2317-2323(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE-21608551; PubMed-11743194;
RA      Goodner B., Hinkle G., Gattling S., Miller N., Blanchard M.,
RA      Goudello B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA      Houmel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
RA      Wollam C., Allinger M., Doughy D., Scott C., Lapps C., Marfeiz B.,
RA      Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA      Clelo C., Slater S.;
RT      Genome sequence of the plant pathogen and biotechnology agent
RT      Agrobacterium tumefaciens C58.
RL      Science 294:2323-2328(2001).
DR      EMBL; AE009102; AAL42421.1; -
DR      EMBL; AE008067; AAK87207.1; -
KW      Complete proteome.
SQ      SEQUENCE 257 AA; 26622 MW; FF7A61FCA4B2B5C CRC64;

Query Match      49.4%; Score 644; DB 16; Length 257;
Best Local Similarity 51.7%; Pred. No. 8.1e-37;
Matches 134; Conservative 41; Mismatches 76; Indels 8; Gaps 3;

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Qy      243 NPFINGEVIRLDGAIKMP 261
        |||:|
Db      238 NDYNGEVIRLDGAIKMP 256

RESULT 14
ID      09DCX5      PRELIMINARY;      PRT;      126 AA.
AC      09DCX5;
DT      01-JUN-2001 (TREMBlrel. 17, Created)
DT      01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Hydroxyacyl-coenzyme A dehydrogenase, type II.
GN      HSD17B10 OR HADH2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX      MEDLINE-21085660; PubMed-11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barz G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA      Brownstein M.C., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hune D.A., Kamuya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA      Wyszynski A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA      Hayashizaki Y.;
RT      Functional annotation of a full-length mouse cDNA collection.
RL      Nature 409:685-690(2001).
-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
      (SDR) FAMILY.
DR      EMBL; AK002368; BAB22046.1; -
DR      HSSP; 070351; 1B6M.
DR      MGD; MGI:1333871; Hsd17b10.
DR      InterPro; IPR002198; ADH_short.
DR      Pfam; PF00106; adh_short; 1.
DR      PRINTS; PR00080; SDRFAMILY.
DR      PROSITE; PS00061; ADH_SHORT; 1.
KW      Oxidoreductase.
SQ      SEQUENCE 126 AA; 13265 MW; 78FBE6D441B9989D CRC64;

Query Match      46.7%; Score 609; DB 11; Length 126;
Best Local Similarity 95.2%; Pred. No. 8.8e-35;
Matches 120; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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RESULT 15
08T217

RT Sinorhizobium meliloti pSyma megaplasmid.
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL: AE007266; AAK65450.1; -.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 255 AA; 26329 MW; ED6C7942D3ED867C CRC64;

Query Match 51.5%; Score 672; DB 16; Length 255;
 Best Local Similarity 54.7%; Pred. No. 9.5e-39;
 Matches 139; Conservative 34; Mismatches 79; Indels 2; Gaps 1;

QY 8 VGLVAIVTGGASGLATAEERLVGQASAVLLDLPNSGGEAAKKGNNCFAPADYTS 67
 DB 3 LKSRFTIVTGASSGCAAVTRMLAOGATVGLDLKPPAGEPEPAELGAAYFRNADYTN 62
 QY 68 EKDVOTALAKGKRGVDVAVNCAAGIAVASKTYMKKGQTHLEDFORVLDVNLNGTEN 127
 DB 63 EADATALLAFKQERGHVAGLVNCACTAGEKI--LGSSGPRALDSFARTVAVNLIGTFN 120
 QY 128 VIRLVAGENGQNEPDGGGQGVIIINTASYAAFEQGVQGAAYASASKGIVGMLTPIARDLA 187
 DB 121 MIRLAEEVNSGCEPDGDERGVIVNTASTAIFDQIGQAAVYASKGVAAALTLPAARELA 180
 QY 188 PIGIRMTIAPGLFGTPLLTLSPKRYANFLASQVPPPSLGDPAEYAHVQAIIENPPLN 247
 DB 181 REIRRVYTLAPGFEDPMAGMPQDVODALLASVPPPLGAEYEAALVKHICENTMLN 240
 QY 248 GEVIRLDGAIKMP 261
 DB 241 GEVIRLDGAIKMP 254

RESULT 11

Q98HMA PRELIMINARY; PRT; 253 AA.

ID Q98HMA; AC Q98HMA; RT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE 3-hydroxycy1-coA dehydrogenase type II.
 GN MKR2603.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Pyllobacteriaceae; Mesorhizobium.
 NCBI_Taxid=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAF303099;
 RX MEDLINE=21082930; PubMed=11114968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Matanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003000; BAB49842.1; -.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 253 AA; 25814 MW; 8832D90EB9BD3D2A CRC64;

Query Match 51.3%; Score 669; DB 16; Length 253;
 Best Local Similarity 54.4%; Pred. No. 1.5e-38;
 Matches 137; Conservative 37; Mismatches 74; Indels 4; Gaps 2;

QY 10 GLVAIVTGGASGLATAEERLVGQASAVLLDLPNSGGEAAKKGNNCFAPADYTSK 69
 DB 5 GQIAIVTGGSSGGEAARALAAKARVALFEDVIGIEAAKVAADIG--ISVGVDSAD 62
 QY 70 DVCTALALAKGKRGVDVAVNCAAGIAVASTYMLKKQTHLEDFORVLDVNLNGTFNY 129
 DB 63 SGTAALAEASKGEPRIILVNCAGIAIGVET--IGKDGPPLDQYKRVIEVNLIGTFNMI 120
 QY 130 RLVAGENGQNEPDGGGQGVIIINTASYAAFEQGVQGAAYASASKGIVGMLTPIARDLPI 189
 DB 121 RLVADRAASLEPLQGGSGRGVIVNTASTAAYDQIGQAAVYASKGVGMLTPIARDLARS 180
 QY 190 GIRMTIAPGLFGTPLLTLSPKRYANFLASQVPPPSLGDPAEYAHVQAIIENPPLNGE 249
 DB 181 GIRVCTIAPGIFKIPMAGMPQDVODSLGAIVPPPSLGESEYEAALAHILNOMLNGE 240
 QY 250 VIRLDGAIKMP 261
 DB 241 TIRLDGAIKMP 252

RESULT 12

Q9AHY1 PRELIMINARY; PRT; 255 AA.

ID Q9AHY1; AC Q9AHY1; RT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
 DE FADB2x.
 GN FADB2x.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NCBI_Taxid=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=U;
 RX MEDLINE=21150437; PubMed=11251808;
 RA Oliveira E.R., Carneiro D., Garcia B., Minambres B., Moreno M.A.,
 RA Canejo L., DiRusso C.C., Naharro G., Irujo J.M.;
 RT "Two different pathways are involved in the b-oxidation of n-alkanoic
 and n-phenylalkanoic acids in Pseudomonas putida U: genetic studies
 and biotechnological applications";
 RL Mol. Microbiol. 39:863-874(2001).
 CC -1. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SCR) FAMILY.
 DR EMBL: AF290950; AAK18170.1; -.
 DR HSSP: O70351; 1E3S.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 255 AA; 26003 MW; 56B658DE906E73F CRC64;

Query Match 50.2%; Score 654; DB 2; Length 255;
 Best Local Similarity 54.5%; Pred. No. 1.6e-37;
 Matches 134; Conservative 40; Mismatches 70; Indels 2; Gaps 1;

QY 14 VITGASGLATAEERLVGQASAVLLDLPNSGGEAAKKGNNCFAPADYTSKDVOT 73
 DB 9 IVSGAASGLGATQMLVEGAKMVLVDLNAQVAEAKARRELGDARPAVADISDEQAQA 68
 QY 74 ALALAKGKRGVDVAVNCAAGIAVASTYMLKKQTHLEDFORVLDVNLNGTFNVRLVA 133
 DB 69 AYDAVASFGSLQGLVNCAGIVGAERV--LGKQSPHGLAFARVAVNVLGSEFNLRLAA 126
 QY 134 GEMQNGNEPDGGGQGVIIINTASYAAFEQGVQGAAYASASKGIVGMLTPIARDLPIGRV 193
 DB 127 AAMAGAADENGEGGVIIINTASTAAYDQIGQAAVYASKKAISLTLPAARELARGIRV 186
 QY 194 MTIAPGLFGTPLLTLSPKRYANFLASQVPPPSLGDPAEYAHVQAIIENPPLNGEYIRL 253

OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Margenot S.,
 Arlat M., Billault A., Brothier P., Camus J.C., Cattolico L.,
 Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."
 RL Nature 415:497-502(2002).
 DR EMBL: AL646070; CAD16241.1; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Oxidoreductase; Complete proteome.
 KM SEQUENCE 252 AA; 25642 MW; D6BEACDA9179DF CRC64;
 SQ
 Query Match 53.0%; Score 691.5; DB 16; Length 252;
 Best Local Similarity 57.1%; Pred. No. 4,3e-40;
 Matches 145; Conservative 33; Mismatches 71; Indels 5; Gaps 3;
 OY 8 VKGLVAVITGASGGLATFAERLVGQASAVLLDLPNSGGEQAARKIGNCVFAPADVT 67
 DB 3 IRQGVITVGASGLAGTTRALAEGRVVIADLNEAGALADEIGER--FVRCDVSS 60
 OY 68 EKDVOITALAKGKGRVDVAVNCAGIAVASKTYMLKKGQHTLEDFOFVLDVNMGTFFN 127
 DB 61 EADGQAAYOAR-SIGALAGLVNCAGIAPASRT--VGKAGPHLPDQFAVININILGFEN 117
 OY 128 VIRLVAGENGQEPDGGRGVYIINTASVAFEQVGAASASGKGIYGMTLPARDLA 187
 DB 118 MIRLAATMTANAFNAGRGVYIINTASVAAPDGGQGAAYASGAGVATLARIADLS 177
 OY 188 PIGIRVMTAPGLFGLTSLPEKAVANFLASQVPPPSRLGDPAEYAHLYOAIENPFLN 247
 DB 178 RQDIRVMTAPGLFGLTSLPEKAVANFLASQVPPPSRLGDPAEYAHLYOAIENPFLN 237
 OY 248 GEVIRLDGAIRMP 261
 DB 238 GETIRLDGAIRMP 251

RESULT 9

O06544 PRELIMINARY; PRT; 250 AA.
 AC 006544;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Oxidoreductase, short-chain dehydrogenase/reductase family.
 GN RV1144 OR MTC165.11 OR M11177.
 OS Mycobacterium tuberculosis.
 OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
 OC Actinomycetales: Corynebacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala K.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
 Hornby T., Jagels K., Kirog A., McLean J., Moule S., Murphy L.,
 Oliver S., Osborne K., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 complete genome sequence."

RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J.F., DeBoy R., Dodson R., Gwinn M.U., Haft D., Hickey E.,
 Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA DeLong A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 laboratory strains."
 RL Submitted (Apr-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: U95584; CAB09032.1; -
 DR EMBL: AE006996; AAK45436.1; -
 DR HSP: O70351; 1E3S.
 DR TIGR: MT1177; -
 DR TubercuList; RV1144; -
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short.1.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Hypothetical protein; Complete proteome.
 KM SEQUENCE 250 AA; 25787 MW; 123A1005A12BD66 CRC64;
 SQ

Query Match 51.6%; Score 673.5; DB 16; Length 250;
 Best Local Similarity 60.1%; Pred. No. 7,3e-39;
 Matches 152; Conservative 25; Mismatches 69; Indels 7; Gaps 4;

OY 9 KGLVAVITGASGGLATFAERLVGQASAVLLDLPNSGGEQAARKIGNCVFAPADVTSE 68
 DB 4 KDAVAVITGASGGLATTKRLDLGAGQVYVD--RGDDVYGLDPRFAQADVTDE 60
 OY 69 KDVOITALAKGKGRVDVAVNCAGIAVASKTYMLKKGQHTLEDFOFVLDVNMGTFFN 128
 DB 61 AAVSNALBLA-DSGPRVAVVNCAGTGAIV--LSRDGVPLAFAKIVDINLVGFNV 117
 OY 129 IRLVAGENGQEPDGGRGVYIINTASVAFEQVGAASASGKGIYGMTLPARDLA 188
 DB 118 LRLGERTAKTEP-IGERGVIYINTASVAAPDGGQGAAYASGAGVATLARIADLS 176
 OY 189 IGIRVMTAPGLFGLTSLPEKAVANFLASQVPPPSRLGDPAEYAHLYOAIENPFLN 248
 DB 177 KLIRVMTAPGLFGLTSLPEKAVANFLASQVPPPSRLGDPAEYAHLYOAIENPFLN 236
 OY 249 EVIRLDGAIRMP 261
 DB 237 EVIRLDGAIRMAP 249

RESULT 10

O02YSL1 PRELIMINARY; PRT; 255 AA.
 AC 002YSL1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Probable.
 GN RA0792 OR SMA1452.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid psyma (megaplasmid 1).
 OC Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 Bartley Huber F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 KA Khan S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yen K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire

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QY 123 MGTFVIRLVAGMGONPEPDGORGVIINTASVAAFEGOVGAAYASASKGIVGMTLP 182
DB 120 LGTFVIRLVAGMGONHEKDANGORGVIINTASVAAPDQGTQASYSASKGIVGMTLP 179
QY 183 ARDLAPIGIRVMTIAPGLFETPLTSLPEKVANFLASQVPPFSRIGDAEYAHVQAITE 242
DB 180 ABDFADGIRFMTIAPGLMDTPLLSSLPKVSFLAQLIPLNPSRLGHPHEYGALVQHITE 239
QY 243 NPFLNGEVRILDAIRM 259
DB 240 NOYLNGEVRILDAIRM 256

RESULT 6
Q910T0 PRELIMINARY; PRT; 255 AA.
ID C910T0;
AC C910T0;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2002 (TRENBLREL. 16, Last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Probable short-chain dehydrogenase.
GN PA2354.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou Y.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL: AE004683; AAC05942.1; -.
DR HSSP: C70351; 1E3S.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Oxidoreductase; Complete proteome.
SQ SHQUNE 255 AA; 26426 MW; EB8FF2871D2936D CRC64;

Query Match 55.4%; Score 722; DB 16; Length 255;
Best Local Similarity 57.5%; Pred. No. 3.5e-42;
Matches 145; Conservative 39; Mismatches 66; Indels 2; Gaps 1;

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RESULT 7
Q8YBS0 PRELIMINARY; PRT; 255 AA.
ID Q8YBS0;
AC Q8YBS0;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE 3-oxoacyl-(acyl-carrier protein) reductase (EC 1.1.1.100).
GN BME10816.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / B10TYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapatal V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lydids A., Reznik G.,
RA Jalonoski L., Larsen N., D'Souza W., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Teveson J.J.,
RA Haselkorn R., Kyrides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL: AE009715; AAL54058.1; -.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KM Oxidoreductase; Complete proteome.
SQ SEQUENCE 255 AA; 26263 MW; 5CF61D4B37FEB730 CRC64;

Query Match 54.7%; Score 713; DB 16; Length 255;
Best Local Similarity 57.1%; Pred. No. 1.5e-41;
Matches 144; Conservative 37; Mismatches 69; Indels 2; Gaps 1;

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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glassi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudt F., Suzuki K., Tomita K., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Morone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata T., Storch K.F.,
 RA Suzuki K., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDS) FAMILY
 CC EMBL: AK013340; BAB28800.1; -
 DR HSSP: 070351; 1E6W.
 DR MGD: MGI:1333871; Hsd17b10.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR OXIDOREDUCTASE.
 KW SEQUENCE 261 AA; 27273 MW; F36CD179C7FCEFAF CRC64;

Query Match 88.6%; Score 1155; DB 11; Length 261;
 Best Local Similarity 87.4%; Pred. No. 6.4e-72;
 Matches 228; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAACSVKGLVAVITGGASGLATAERLVGGASAVLLDLPNSGGEQAQKLNCF 60
 DB 1 MAASVSVKGLVAVITGGASGLATAERLVGGASAVLLDLPNSGGEQAQKLESCIF 60
 QY 61 APADYSEKDVQFALALAKGKRGVAVYAVNCAGIAVASKTYNLKKGOTHTLEDFORVLDV 120
 DB 61 APANVSEKEIOALALAKKEXFERIDVAVNCAGIAVAITYNHOKKKHTLEDFORVINV 120
 QY 121 NLGTRNVITLVAGKQNEPDGQGRVITINTASVAEEGQGAASASGVIQMTL 180
 DB 121 NLGTRNVITLVAGKQNEPDGQGRVITINTASVAEEGQGAASASGVIQMTL 180
 QY 181 PIRADLPAGIRVMTAPGLFGTPLTSLPEKAVNFASQVPPSRLLGPAEVAHLVCAI 240
 DB 181 PIRADLPAGIRVMTAPGLFGTPLTSLPEKAVNFASQVPPSRLLGPAEVAHLVCAI 240
 QY 241 IENPFLNGEYIRLDGAIKMP 261
 DB 241 IENPFLNGEYIRLDGAIKMP 261

RESULT 4
 O8TCV9 PRELIMINARY; PRT; 196 AA.
 AC O8TCV9;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Endoplasmic reticulum-associated amyloid beta peptide-binding protein
 DE (Fragment).
 GN ERB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Deininger M.H., Meyerman R., Schluesener H.J.;
 RT "Expression, release and induction of endoplasmic reticulum-associated
 amyloid beta-binding protein in brain disease."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY092415; AAM18189.1; -
 FT NON_TER 1
 FT 196
 SO SEQUENCE 196 AA; 20581 MW; 240DE149665AA6A CRC64;
 Query Match 75.5%; Score 984; DB 4; Length 196;
 Best Local Similarity 99.5%; Pred. No. 2.6e-60;
 Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 51 AKKGNVCVPAADVTSEKDVQFALALAKGKRGVAVYAVNCAGIAVASKTYNLKKGOTHT 110
 DB 1 AKKGNVCVPAADVTSEKDVQFALALAKGKRGVAVYAVNCAGIAVASKTYNLKKGOTHT 60
 QY 111 LEDEFORVLDVNLGTFENVIRLVAGKQNEPDGQGRVITINTASVAEEGQGAAYSA 170
 DB 61 LEDEFORVLDVNLGTFENVIRLVAGKQNEPDGQGRVITINTASVAEEGQGAAYSA 120
 QY 171 SKGIVGKTLPIADLPAGIRVMTAPGLFGTPLTSLPEKAVNFASQVPPSRLLGDP 230
 DB 121 SKGIVGKTLPIADLPAGIRVMTAPGLFGTPLTSLPEKAVNFASQVPPSRLLGDP 180
 QY 231 AEVAHLVCAIENPFL 246
 DB 181 AEVAHLVCAIENPFL 196

RESULT 5
 Q19102 PRELIMINARY; PRT; 258 AA.
 AC Q19102;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Probable 3-hydroxyacyl-CoA dehydrogenase F01G4.2 type II (EC 1.1.1.35)
 DE (Type II HADH).
 DE F01G4.2.
 GN Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Rhabditidae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Harris B.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +
 NADH.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 FAMILY (SDR).
 CC EMBL: 268341; CAA92764.1; -
 DR HSSP: 070351; 1E6W.
 DR WormPep: F01G4.2; CE03127.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 DR Hypothetical protein; Oxidoreductase; NAD; Mitochondrion.
 KW ACT_SITE 11
 FT NP_BIND 36
 FT ACT_SITE 165
 SO SEQUENCE 258 AA; 27143 MW; 86BF2568EE6902B3 CRC64;

Query Match 57.5%; Score 750; DB 5; Length 258;
 Best Local Similarity 59.9%; Pred. No. 4.2e-44;
 Matches 154; Conservative 34; Mismatches 67; Indels 2; Gaps 1;
 QY 3 AACRSYKGLVAVITGGASGLATAERLVGGASAVLLDLPNSGGEQAQKLNVCVAP 62
 DB 2 SALRSTKGLVAVITGGASGLATKGAQVAVIIDLPGSKGADVAKETIG--ITP 59
 QY 63 AAVTSEKDVQFALALAKGKRGVAVYAVNCAGIAVASKTYNLKKGOTHTLEDEFORVLDVNL 122
 DB 60 AAVTSEKDVQFALALAKGKRGVAVYAVNCAGIAVASKTYNLKKGOTHTLEDEFORVLDVNL 119

```

90 286.5 22.0 246 2 Q9RB80 Q9rb80 burkholderi
91 286.5 22.0 246 2 Q9F519 Q9f519 streptomyce
92 286.5 22.0 256 17 Q9RT15 Q9rt15 methanosarc
93 286 21.9 252 16 Q9ZP0 Q9zp0 rhizobium m
94 285.5 21.9 257 16 Q9WYD3 Q9wyd3 thermotoga
95 285 21.9 255 16 Q9PCQ2 Q9pcq2 xyloella fas
96 285 21.9 317 10 Q93X68 Q93x68 brassica na
97 284.5 21.8 253 16 Q9CH41 Q9ch41 lactococcus
98 284.5 21.8 272 16 Q99R31 Q99r31 staphylococ
99 284 21.8 275 16 Q9K4H0 Q9k4h0 streptomyce
100 283 21.7 258 16 Q99X89 Q99x89 staphylococ

```

ALIGNMENTS

```

RESULT 1
Q96HD5 PRELIMINARY: PRT: 252 AA.
ID Q96HD5;
AC Q96HD5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE Similar to hydroxycyl-coenzyme A dehydrogenase, type II.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Straussberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL: BC008708; AA08708.1; -.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase.
SQ SEQUENCE 252 AA; 25984 MW; F36B371070CE872D CRC64;

```

Query Match 95.2%; Score 1241.5; DB 4; Length 252;

Best Local Similarity 96.2%; Pred. No. 7e-78; Matches 251; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

```

QY 1 MAACRSYKGLVAVITGGASGLGATAPRLVGGASAVLLDPNSGGEAOKKLGNNCVF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAPRLVGGASAVLLDPNSGGEAOKKLGNNCVF 60
QY 61 APADVTSEKDYOTALAKGKFGKRVDAVNCAGIAVASKTYNLKQGTHTLEDFOQRYLDV 120
DB 61 APADVTSEKDYOTALAKGKFGKRVDAVNCAGIAVASKTYNLKQGTHTLEDFOQRYLDV 120
QY 121 NLMGTFNIVRLVAGMGONPEPDGQGRVITINTASVAAPFGQGAAYSAKSGIVGML 180
DB 121 NLMGTFNIVRLVAGMGONPEPDGQGRVITINTASVAAPFGQGAAYSAKSGIVGML 180
QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYNFLASQVPPSRGLDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYNFLASQVPPSRGLDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261
QY 252 IENPFLNGEVIRLDGAIKMP 252
DB 252 IENPFLNGEVIRLDGAIKMP 252

```

RESULT 2

```

Q99N15 PRELIMINARY: PRT: 261 AA.
ID Q99N15;
AC Q99N15;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)

```

```

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Short chain L-3-hydroxycyl-CoA dehydrogenase.
GN HSD17B10 OR SCHAD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21096701; Pubmed=11165016;
RA He X.Y., Merz G., Chu C.H., Lin D., Yang Y.Z., Mehta P., Schulz H.,
RA Yang S.Y.;
RT "Molecular cloning, modeling, and localization of rat type 10 17beta-
RT hydroxysteroid dehydrogenase."
RU Mol. Cell. Endocrinol. 171:89-98(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC EMBL: AF233685; AA015008.1; -.
DR HSP: 070351; I66W.
DR MGD: MG1:133871; Hsd17b10.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short.1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 261 AA; 27273 MW; F371ED8A15CECFMF CRC64;

```

Query Match 89.9%; Score 1159; DB 11; Length 261;

Best Local Similarity 87.7%; Pred. No. 3.4e-72; Matches 229; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

```

QY 1 MAACRSYKGLVAVITGGASGLGATAPRLVGGASAVLLDPNSGGEAOKKLGNNCVF 60
DB 1 MAACRSYKGLVAVITGGASGLGATAPRLVGGASAVLLDPNSGGEAOKKLGNNCVF 60
QY 61 APADVTSEKDYOTALAKGKFGKRVDAVNCAGIAVASKTYNLKQGTHTLEDFOQRYLDV 120
DB 61 APADVTSEKDYOTALAKGKFGKRVDAVNCAGIAVASKTYNLKQGTHTLEDFOQRYLDV 120
QY 121 NLMGTFNIVRLVAGMGONPEPDGQGRVITINTASVAAPFGQGAAYSAKSGIVGML 180
DB 121 NLMGTFNIVRLVAGMGONPEPDGQGRVITINTASVAAPFGQGAAYSAKSGIVGML 180
QY 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYNFLASQVPPSRGLDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKYNFLASQVPPSRGLDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMP 261
DB 241 IENPFLNGEVIRLDGAIKMP 261

```

RESULT 3

```

Q9CYT3 PRELIMINARY: PRT: 261 AA.
ID Q9CYT3;
AC Q9CYT3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Hydroxycyl-coenzyme A dehydrogenase, type II.
GN HSD17B10 OR HADH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawal J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

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Thu Jun 26 06:55:05 2003

us-09-931-186-20.rspt

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:22:37 ; Search time 31.6667 Seconds
(without alignments)
1698.262 Million cell updates/sec

Title: US-09-931-186-20
Perfect score: 1304
Sequence: 1 MAACRSYKGLVAVITGGAS.....ENPLNGEVRLDGAIRMQP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_UNCLASSIFIED:*
14: SP_VIRUS:*
15: SP_BACTERIAP:*
16: SP_ARCHAEA:*
17: SP_ARCHAEA:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	1241.5	95.2	252	4	Q96HD5	Q96HD5 homo sapien
2	1159	88.9	261	11	Q99N15	Q99N15 mus musculu
3	1155	88.6	261	11	Q9CYT3	Q9CYT3 mus musculu
4	984	75.5	196	4	Q8TVC9	Q8TVC9 homo sapien
5	750	57.5	258	5	Q19102	Q19102 caenorhabdi
6	722	55.4	255	16	Q910T0	Q910T0 pseudomonas
7	713	54.7	255	16	Q81BS0	Q81BS0 bruceella me
8	691.5	53.0	252	16	Q8XWEO	Q8XWEO ralsstonia s
9	673.5	51.6	250	16	Q06544	Q06544 mycobacteri
10	672	51.5	255	16	Q92YS1	Q92YS1 rhizobium m
11	669	51.3	253	16	Q98BM4	Q98BM4 rhizobium l
12	654	50.2	255	2	Q9AHY1	Q9AHY1 pseudomonas
13	644	49.4	257	16	Q8UFI2	Q8UFI2 agrobacteri
14	609	46.7	126	11	Q9DCX5	Q9DCX5 mus musculu
15	603.5	46.3	264	5	Q8T2L7	Q8T2L7 dictyostell
16	597	45.8	260	16	Q9ABU6	Q9ABU6 caulobacter

17	386	29.6	443	2	Q935J3	Q935J3 myxococcus
18	375.5	28.8	246	16	Q8XJH1	Q8XJH1 clostridium
19	357.5	27.4	244	16	Q991D6	Q991D6 streptococc
20	355	27.2	252	16	Q9HW15	Q9HW15 pseudomonas
21	345.5	26.5	249	16	Q97DA6	Q97DA6 clostridium
22	339.5	26.0	247	16	Q8R9W0	Q8R9W0 thermotomaer
23	335.5	25.7	246	16	Q9KA03	Q9KA03 bacillus ha
24	335.5	25.7	297	3	Q42774	Q42774 neurospora
25	334.5	25.7	251	16	Q8YWT0	Q8YWT0 anabaena sp
26	332	25.2	246	16	Q9K336	Q9K336 bacillus ha
27	328.5	25.2	248	2	Q9KJF1	Q9KJF1 thauera aro
28	327.5	25.1	260	16	Q88068	Q88068 streptococc
29	327.5	25.1	243	16	Q9FBC3	Q9FBC3 streptococc
30	326.5	25.0	243	16	Q9CHF7	Q9CHF7 lactococcus
31	325	24.9	262	2	Q9L9F8	Q9L9F8 streptomyce
32	324.5	24.9	250	4	Q96KK9	Q96KK9 homo sapien
33	323	24.8	271	10	Q94G09	Q94G09 cucumis sat
34	322	24.7	261	13	Q8U0M4	Q8U0M4 cryzias lat
35	321	24.6	263	16	Q9KYM4	Q9KYM4 streptomyce
36	320.5	24.6	246	2	Q9EX74	Q9EX74 rhodococcus
37	320	24.5	271	10	Q94G10	Q94G10 cucumis sat
38	319.5	24.5	261	6	Q8WMA4	Q8WMA4 macaca mula
39	319	24.5	258	2	Q9F8V0	Q9F8V0 streptomyce
40	317	24.3	299	17	Q97UK6	Q97UK6 sulfolobus
41	316.5	24.3	259	16	Q8U616	Q8U616 agrobacteri
42	316.5	24.3	313	2	Q93HC0	Q93HC0 streptomyce
43	315.5	24.2	296	16	Q9ABX6	Q9ABX6 caulobacter
44	313.5	24.0	240	17	Q9UY54	Q9UY54 pyrococcus
45	313.5	24.0	249	2	Q9ATJ2	Q9ATJ2 thauera aro
46	313	24.0	247	16	Q9PFF6	Q9PFF6 xylella fas
47	313	24.0	262	16	Q81D84	Q81D84 bruceella me
48	312	23.9	237	4	Q8WT8	Q8WT8 homo sapien
49	311.5	23.9	244	16	Q8ZFF5	Q8ZFF5 yeastina pe
50	310.5	23.8	260	17	Q8UB33	Q8UB33 pyrococcus
51	310	23.8	256	16	Q8ZB06	Q8ZB06 yeastina pe
52	310	23.8	267	10	P93697	P93697 vigna ungu
53	309	23.7	253	16	Q8U759	Q8U759 agrobacteri
54	308.5	23.7	247	16	Q8Y690	Q8Y690 listeria mo
55	308.5	23.7	247	2	Q9F5J1	Q9F5J1 streptomyce
56	308.5	23.7	247	2	Q9F5J1	Q9F5J1 streptomyce
57	303.5	23.3	236	11	Q91VT4	Q91VT4 mus musculu
58	303.5	23.3	247	16	Q92AK1	Q92AK1 listeria in
59	303	23.2	247	2	Q9ZFF9	Q9ZFF9 bacillus me
60	302.5	23.2	248	16	Q8U9B5	Q8U9B5 agrobacteri
61	302.5	23.2	249	2	Q9ABG5	Q9ABG5 geobacillus
62	302.5	23.2	263	2	Q955F7	Q955F7 streptomyce
63	300.5	23.0	258	16	Q93339	Q93339 mycobacteri
64	300	23.0	296	5	Q9XX28	Q9XX28 caenorhabdi
65	300	23.0	252	17	Q97UA4	Q97UA4 sulfolobus
66	298	22.9	255	17	Q9HQ41	Q9HQ41 halobacteri
67	298	22.9	260	16	Q9FBN1	Q9FBN1 streptomyce
68	297.5	22.8	254	16	Q92P88	Q92P88 rhizobium m
69	297.5	22.8	267	2	Q9L8G2	Q9L8G2 leifsonia a
70	297.5	22.8	538	2	Q8YV75	Q8YV75 rhizobium s
71	297	22.8	265	16	Q9S2E4	Q9S2E4 streptomyce
72	296	22.7	245	16	Q8YDN1	Q8YDN1 bruceella me
73	294.5	22.6	270	4	Q9URK3	Q9URK3 homo sapien
74	294	22.5	315	10	Q949M3	Q949M3 brassica na
75	294	22.5	320	10	Q93X62	Q93X62 brassica na
76	293.5	22.5	270	4	Q9EPX1	Q9EPX1 homo sapien
77	293	22.5	255	16	Q8RDG3	Q8RDG3 thermotomaer
78	293	22.5	258	16	Q93015	Q93015 rhizobium m
79	293	22.5	328	10	Q93X67	Q93X67 brassica na
80	293	22.5	246	2	Q93HB3	Q93HB3 streptomyce
81	292	22.4	272	16	Q8YHE0	Q8YHE0 rhizobium l
82	291.5	22.4	405	16	Q98AS0	Q98AS0 bruceella me
83	289.5	22.2	254	10	Q949M2	Q949M2 brassica na
84	289.5	22.2	303	10	Q9SCU0	Q9SCU0 arabidopsis
85	288.5	22.1	244	16	Q8X815	Q8X815 escherichia
86	288.5	22.1	245	16	Q8RDH9	Q8RDH9 thermotomaer
87	288	22.0	243	16	Q8RG25	Q8RG25 fusobacteri
88	287.5	22.0	247	2	Q930F0	Q930F0 azotobacter
89	287.5	22.0	254	16	Q9RT26	Q9RT26 deinococcus

disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides anxiolytic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention.

Sequence 288 AA:

Query Match 23.0%; Score 300.5; DB 22; Length 288;
Best Local Similarity 31.5%; Pred. No. 5.3e-21;
Matches 86; Conservative 44; Mismatches 116; Indels 27; Gaps 7;

1 MAACRSYGLVAITGASGLGLTAERLVGQASAVLLDPNSGGEAQAQKLGNNCFV 60
10 MATGR-YAGKAVYVGGGGRGAGIVAFVNSGARVYICDDESGRGLDELPGLI 68
61 AADVTSEKVOATALAKKRGVDVAVNCAGIVASTYLNKGGTHLEDFORVLDV 120
69 SCQDVQEDDVLTSETIRFRGRDCCVNNAGHPP-ORPEETSAHGFRQLLEL 123
121 NIMGFENVIRLVAGGQNEPDGQGRGVIINTASVAAFEGVGQAASASKSGIVGTL 180
124 NLGTTTLTKLALPYARKSQ-----GVNINISSLVGAGCAQANPVATGANTMTK 176
181 PIARDLAPGIRVMTAPLFGTPLTSL-PEKVA---NFLAS-----QVFPSERL 227
177 AALDESPYGVVNCISPCNINMTPLMEELALALPDPRIIRBGLAAGRSQVGIOLPLRM 236
228 GDPAEY-AHLVQAIIENPFLNGEVIRLDGAIIM 259
237 GDPAEVGAANVFLASBANFCTGIXLVTGAEI 269

RESULT 24
ABP39667
ID ABP39667 standard; Protein: 263 AA.

AC ABP39667;

DT 24-JUL-2002 (first entry)

DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4512.

KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
antibacterial; gene therapy.

OS Staphylococcus epidermidis.

PN US6380370-B1.

PD 30-APR-2002.

PF 13-AUG-1998; 98US-0134001.

PR 14-AUG-1997; 97US-055779P.

PR 08-NOV-1997; 97US-064964P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Doucette-Stamm LA, Bush D;

DR WPI, 2002-381255/41.

DR N-PSDB; ABN92212.

PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis
polypeptide, useful for diagnosing and treating bacterial infections -

PS Disclosure; SEQ ID 4512; 267pp; English.

CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
frame (ORF) nucleic acid sequences which encode the amino acid sequences
given in ABP3124 to ABP3960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences
can also be used in the diagnosis and treatment of bacterial infections,
particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life
cycle or inhibit S. epidermidis infection.
CC N.B. The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from the
USPTO web site.

Sequence 263 AA:

Query Match 22.9%; Score 298; DB 23; Length 263;
Best Local Similarity 32.3%; Pred. No. 8.2e-21;
Matches 85; Conservative 43; Mismatches 107; Indels 28; Gaps 6;

12 VAVITGASGLGLTAERLVGQASAVLLDPNSGGEAQAQKLGNNCFV 68
11 VAVITGAAGIGLTAERLVGQASAVLLDPNSGGEAQAQKLGNNCFV 70
69 KDVOATALAKKRGVDVAVNCAGIVASTYLNKGGTHLEDFORVLDVIMGFENV 128
71 DVQSVLVNQQVEHGDNLVNNAGLGPMTPI-----ESVTEQFQNVGVGVFWG 124
129 IRLVAGMGQNEPDGQGRGVIINTASVAAFEGVGQAASASKSGIVGTLPIARDLAP 188
125 IQAAIEGP-----DKLHGKILNATSOAGVEGNAGLSLSTFAVRLTQVAARDLAE 179
189 IGRVMTAPLFGTPLTSLPEKVA-----NFLASQVFPSERLDGPAAVAVLV 237
180 KNIVVNAFAPGIVETPMKKGIAXELABENNQPMWGWKQFTDIAL-KRLSKPEDVAVV 238
238 QAIL--ENPFLNGEVIRLDGAIIR 258
239 SFLAGSDSDYITGQTIIVDGMR 261

RESULT 25
AAB47459
ID AAB47459 standard; Protein: 267 AA.

AC AAB47459;

DT 13-DEC-2001 (first entry)

DE Levodione reductase.

KW Levodione reductase; homologous subunit; levodione; primer; amplify;
(4R,6R)-4-hydroxy-2,2,6-trimethylcyclohexanone; actinol; zeaxanthin;
PCR; polymerase chain reaction.

OS Corynebacterium aquaticum.

PN EP122315-A1.

PD 08-AUG-2001.

PF 29-JAN-2001; 2001EP-0101940.

PR 01-FEB-2000; 2000EP-0101665.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Shimizu S, Wada M;

DR WPI, 2001-551347/62.

DR N-PSDB; AAB43285.

PT New Corynebacterium aquaticum levodione reductase gene, useful for

DR N-PSDB; AAA89187.
XX
PT New human oxidoreductase proteins useful for diagnosing, treating or
PT preventing proliferative, neurological, genetic, smooth muscle,
PT autoimmune or inflammatory disorders associated with abnormal
PT expression of oxidoreductase proteins
XX
PS Claim 1(a): Page 83; 95pp; English.
XX
CC The present sequence is that of human oxidoreductase OXR-3, as
CC deduced from a cDNA clone (see AAA89187) isolated from a lung tumour
CC cDNA library. The protein shows homology to Escherichia coli
CC 3-oxoacyl-(acyl)-carrier protein, and includes a short-chain
CC dehydrogenase signature. OXR-3 is expressed in nervous, reproductive,
CC cardiovascular and gastrointestinal tissue, and may be involved in
CC cell proliferation and inflammation. The invention provides OXR-1
CC to 8 polypeptides (see AAB19926-33) and polynucleotides (see
CC AAA89185-92). It also provides methods for using these polypeptides
CC and polynucleotides for diagnosing, treating or preventing disorders
CC associated with expression of OXR, especially cell proliferative,
CC neurological, genetic, smooth muscle, and autoimmune/inflammatory
CC disorders. The proteins can also be used to screen for agonists
CC and antagonists useful for treating these conditions, while
CC antibodies that bind to OXR may be used for diagnosis or in assays
CC to monitor patient treatment.
XX
SQ Sequence 237 AA;
XX
Query Match 23.9%; Score 312; DB 22; Length 237;
Best Local Similarity 31.6%; Pred. No. 3.1e-22;
Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;
QY 12 VAVITGASGLIATRIERLVGGASAVLIDLPNSGGEAAKLGNVCVAPADVTSEKV 71
DB 4 VCAVFGSGSIRGAVNAQIMARKGYRLAVARNLEGAAGAAGLGGDHAFSCDVAKEDV 63
QY 72 QVALAKKGFGRVDVAVNCAGI-----AVASKTYNLKKGQHTDEDFQRVLDVLMGTG 126
DB 64 QNTFEMEKLHGRVNLVNAAGINDGLLYRTK-----EDWVSCILHTLDSM 112
QY 127 NVIRLVAGMGONEPDGGQSGVITNTASVAAFEGVQQAASASAGKGVKTLPIARDL 186
DB 113 LICKAMRTMIDQ-----QGGSIYVGSIVGLKGNSSQSVASASAGKGLVPSRALAKEV 166
QY 187 APIGIRVMTIAPGLGETPLTSLPEKVANFLASQVFPSPRLGDPREVAHLVQATLENRL 246
DB 167 ARKRIYVNVAVPQFVHTMTKDLKEE--HLKKNIPL-GRFOETLEVAAHVAVFLESPTI 222
QY 247 NSEVIRLDDAIRM 259
DB 223 TGHVLYVDGLOL 235
RESULT 21
ABBA8892
ID ABBA8892 standard; Protein; 247 AA.
XX
AC ABBA8892;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #1596.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX vitamin B12; bacterial infection; disease.
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.

XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTER.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusnlok C, Eshti H, Dehoux P,
PI Dussurget O, Chetouiann F, Nedjati H, Glaser P, Kunst F, Cossart P,
PI Daniels J, Goebel W, Kieft U, Kuhn M, Ng E, Vazquez-Boland JA,
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A,
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L,
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N,
PI Maqueda E, De Paulos B, Wehland J, Kaerst U, Ertlan K, Hauf J,
PI Rose M, Voss H;
XX
WP: 2002-010914/01.
XX
DR Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and
XX related polypeptides -
XX
PS Claim 6; SEQ ID No 1597; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded from the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms,
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 247 AA;
XX
Query Match 23.4%; Score 305.5; DB 23; Length 247;
Best Local Similarity 32.0%; Pred. No. 1.4e-21;
Matches 85; Conservative 45; Mismatches 103; Indels 33; Gaps 7;
QY 7 SVKGLVAVITGASGLIATRIERLVGGASAVLIDLPNSGGEAAQ-----KLT-----GNNC 58
DB 2 TLQGVAVVVGSGSIRGDIATNLAKGANIFF-----NYNGSPAEETKLVAEHGV 57
QY 59 VFAPADVTSEKDVQVALAKKGFGRVDVAVNCAGIYVASKTYNLKKGQHTLEDFQRV 118
DB 58 EAMKANVAIEDVDVAFKQAIERFGRVLDLVNNGITRDILNRKE-----DEMDVYI 111
QY 119 DVNIMCTFNVIIRLVAGMGONEPDGGQSGVITNTASVAAFEGVQQAASASAGKGV 178
DB 112 NINLKGFTCKVNSRTMMKQ-----RAKKIINMASVGLLIGNAGANVYAKAGVIGL 165
QY 179 TLPARLAPIGITVMTIAPGLGETPLTSLPEKVANFLASQVFPSPRLGDPREVAHLVQ 238
DB 166 TKTLARLAPRGIVNVAVPQFVHTMTKDLKTKRAMLAQIP---LGAVGTTEIDIAN 221
QY 239 AII-----ENPFLNGEVIRLDDAIRM 259
DB 222 AVLFASDASKYITIGQTLSDVGGVM 247
RESULT 22
AA95746
ID AA95746 standard; Protein; 247 AA.
XX
AC AA95746;

XX 18-DEC-2001 (first entry)
 XX Novel human secretory protein, Seq ID No 325.
 DE
 XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KM Ischemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KM Transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KM Amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KM Ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KM Gut protection; lung; liver fibrosis; immune deficiency; infection;
 KM Severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KM Multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KM Fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 PN MO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0683563.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 DR WPI; 2001-589934/66.
 DR N-PSDB; AAS45056.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Example 4; SEQ ID No 325; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing hematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides

CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 CC
 XX
 SQ Sequence 237 AA;
 Query Match 23.9%; Score 312; DB 22; Length 237;
 Best Local Similarity 31.6%; Pred. No. 3.1e-22;
 Matches 80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;
 QY 12 VAVITGASGIGLTAERLVQGGASAVLLDPNNGSGSAQKKNVFAFAPVTSKQV 71
 DB 4 VCAVFGSGRGIGRAVQAQMARKGYRLAVIARNEGARAAGDLAGDHLAFSCVAKEDV 63
 QY 72 QTAALAKGKPRYDVAVNCAGI-----AAASKTYNKKGQTHLTEDFQVLVDNLMGTF 126
 DB 64 QNTFEEKEKHLGRVNFVNNAGINRDGLVTRKT-----EDMVSQHLTNLGSW 112
 QY 127 NVITLVAGEMQNEPDGCGRGVYIINTASVAAPFGVQGAAYSASKSGIGVMTPIARDL 186
 DB 113 LTCRAAMFTMQ-----DGGSTVNGSTVGLKNGSGQSYSAKSGLVGFSAALAKEV 166
 QY 187 APIGIRVNTIAPGLFGTPILTSLPEKYANFLASQVPPSRIGDPAEYAHVQAATIEHPFL 246
 DB 167 ARKIRIVAVAPGVVHDMTKDLKE---HLKKRIPL-GRFGETIEVAHVAVPLESPYI 222
 QY 247 NGEVIRLDGATRM 259
 DB 223 TGHVLVDGGLQL 235
 XX
 XX RESULT 20
 XX AAB19928
 XX ID AAB19928 standard; Protein: 237 AA.
 XX
 XX AAB19928;
 XX
 XX 19-MAR-2001 (first entry)
 XX
 XX Human oxidoreductase OXRD-3.
 XX
 XX OXRD-3; human; oxidoreductase; dehydrogenase; cell proliferation;
 XX neurological disease; smooth muscle disease; autoimmune disease;
 XX inflammation; antiproliferative; neuroprotective;
 XX immunosuppressive; antiinflammatory; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 66 /note="O-phosphorylated"
 FT Misc-difference 95 /note="O-phosphorylated"
 FT Misc-difference 114 /note="O-phosphorylated"
 FT Region 3..184 /note="short-chain dehydrogenase signature"
 FT
 FT WO200071679-A2.
 XX
 XX 30-NOV-2000.
 XX
 XX 19-MAY-2000; 2000WO-US13879.
 XX
 XX 20-MAY-1999; 99US-0135049.
 XX 27-MAY-1999; 99US-0136740.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Yue H, Tang YT, Baughn MR, Lu DM;
 XX WPI; 2001-025146/03.

XX Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
PI Yamamoto RT, Xu HH;
XX WPI: 2001-611495/70.
DR N-PSDB: AAS53167.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3: Seq ID No 10921; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence : 245 AA;

Query Match 24.6%; Score 320.5; DB 22; Length 245;
Best Local Similarity 33.7%; Pred. No. 4.7e-23;
Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;

QY 15 ITGASGIGLTAERLVGGQGSANVLD---LPNSGGDAQKRGNNCFAPADVTSEKD 70
DB 10 ITGTRGIGKVAALFAFAKGANIVNGRSETTPROREIE--FGVKCIGLSGISPDFA 67
QY 71 VOTALAKGKFRGVDVAVNCAGIAVASKTYNLKKQTHLEDFQRYLDVLMGTFWIR 130
DB 68 AGEMQATVDQGSIDILVNNAGIT-----NDKLLMTEDEPNACIDIVLGTFMNQ 121
QY 131 LVAGMGQNEPDQGGQRCVITNTASVAFEGQVQAAYSASKGGIVGHTLPADLPAPIG 190
DB 122 QAVKMMRO-----RSGRITINMASVSGIMNVQANVAAKAGVGGTKSVAREVAPRG 175
QY 191 IRVMTIAPGLFGTPELTSLPERKANFLAQVFPFRGLDPAEYHIVQAIENFELNGEV 250
DB 176 ITCAALAGCFIOTETMTDVLSKVKQMAQPIQI--FGQVEDVATAATFLAKSVYITIGV 234
QY 251 IRLDGAIRM 259
DB 235 VAVDGLVW 243

RESULT 15
AAU28344
ID AAU28344 standard; Protein: 257 AA.

AAU28344;

18-DEC-2001 (first entry)

Novel human secretory protein, Seq ID No 701.

Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
ischemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.

Homo sapiens.

MO200166689-A2.

13-SEP-2001.

05-MAR-2001; 2001WO-US04942.

07-MAR-2000; 2000US-0519705.

19-MAY-2000; 2000US-0574454.

17-JUN-2000; 2000US-0596193.

14-JUL-2000; 2000US-0616847.

19-SEP-2000; 2000US-0665363.

20-OCT-2000; 2000US-0693267.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI Zhao QA, Yang Y, Dymanc RT, Zhang J, Chen R, Xue AJ, Wang J;

WPI: 2001-589934/66.

N-PSDB: AAS45244.

Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis and treatment of
PT cancer, neurological, inflammatory, and autoimmune disorders -

Example 2: SEQ ID No 701; 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I)
CC and polynucleotides (II). (I) and (II) are useful for treating
CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
CC ischemia-reperfusion injury, shock, sepsis, immune responses, and is
CC involved in increasing hematopoiesis, stem cell survival, bone growth
CC and remodeling. (I), (II) and modulators of (II) are useful for
CC prophylaxis or treatment of one or more cancers. (II) is also useful for
CC creating transgenic animals useful for studying the in vivo activities of
CC the polypeptide as well as for studying modulators of the polypeptides.
CC (I) induces the proliferation of neural cells and regeneration of nerve
CC and brain tissue and is useful for the treatment of central and
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis and is useful for creating myeloid
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC tissue growth, and in tissue repair, healing of burns, incisions,
CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
CC disorders, or periodontal disease. Furthermore, (I) is also useful for
CC gut protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, various immune deficiencies and
CC disorders including severe combined immunodeficiency (SCID), bacterial or
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC reactions and conditions, such as asthma or other respiratory problems.
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
CC fertility, metabolism, catabolism, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU28020-AAU28395 represent novel human secreted protein
CC amino acid sequences of the invention.

Sequence 257 AA;

Query Match 24.38; Score 317; DB 22; Length 257;
Best Local Similarity 31.5%; Pred. No. 1.1e-22;

DB 66 ADARKMIDQAIAEIGSVYDVLYNNAGI--TQDTLMKMK-----TEADFEKVLKVNLTGAFNM 119
 QY 129 IRLVAGEMQNEPDGQGRGVIINTASVAAEQGVQQAASKSGIGVMTLPARDLAP 188
 DB 120 TQSVL-----KPMKAREGAIINMSYVGLMGNIGQANVAASKAGLIGFTKSVAREVAS 173
 QY 189 IGIRVMTIAPGLFGTPLTSLPEKVFANFLASOVPPSPRLGDPAEVYAHLYQAIINPFNG 248
 DB 174 RNRVNVYIAPGMIESDNTALISDKIKETLAQIIPM-KEFGQAEQVADLTIVFLAGODYLTG 232
 QY 249 EVIRLDGAI RM 259
 DB 233 QVIAIDGGLSM 243

RESULT 11
 ID AUA37988 standard; Protein; 243 AA.
 AC AUA37988;
 XX 14-FEB-2002 (first entry)
 DT 14-FEB-2002 (first entry)
 DE Streptococcus pneumoniae cellular proliferation protein #417.
 XX
 KW Antisense; prokaryotic cellular proliferation protein;
 KM antibiotic; antibacterial; drug design.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200170955-A2.
 PD 27-SEP-2001;
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 PI WPI; 2001-611495/70.
 DR N-PSDB; AAS55847.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 13581; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes, themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 243 AA;
 QY Query Match 25.2%; Score 328.5; DB 22; Length 243;
 DB Best Local Similarity 35.1%; Pred. No. 77e-24;
 DB Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
 QY 15 ITGASGLGLATLAEVLYGQASAVLLDPNSGGE-----AQAKKIGNNCFAPADYSE 68
 DB 10 ITGSSRIGIGLAIHAKFAQAGANITVL-----NSRGAISEELLAEFSNGIVVPSGVSDP 65
 QY 69 KDYQTLALAKKFGKRGVADVAVNCAGTAVASKTYNLKKGTHTLDEPQVLYDVNLMTGFVY 128
 DB 66 ADARKMIDQAIAEIGSVYDVLYNNAGI--TQDTLMKMK-----TEADFEKVLKVNLTGAFNM 119
 QY 129 IRLVAGEMQNEPDGQGRGVIINTASVAAEQGVQQAASKSGIGVMTLPARDLAP 188
 DB 120 TQSVL-----KPMKAREGAIINMSYVGLMGNIGQANVAASKAGLIGFTKSVAREVAS 173
 QY 189 IGIRVMTIAPGLFGTPLTSLPEKVFANFLASOVPPSPRLGDPAEVYAHLYQAIINPFNG 248
 DB 174 RNRVNVYIAPGMIESDNTALISDKIKETLAQIIPM-KEFGQAEQVADLTIVFLAGODYLTG 232
 QY 249 EVIRLDGAI RM 259
 DB 233 QVIAIDGGLSM 243

RESULT 12
 ID AAM01032 standard; Protein; 243 AA.
 AC AAM01032;
 XX 02-OCT-2001 (first entry)
 DT 02-OCT-2001 (first entry)
 DE CFE 35 protein sequence.
 XX
 KW Antibacterial; vaccine; gene therapy; bacterial cell wall viability;
 KM CFE; CEG; Conserved Essential Gene; bacterial infection;
 KW antisense therapy; antibiotic resistance.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN WO200149721-A2.
 PD 12-JUL-2001.
 PF 29-DEC-2000; 2000WO-US35604.
 PR 30-DEC-1999; 99US-0174089.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Dougherty TJ, Pucci MJ, Dougherty BA, Davison DB, Bruccoleri RE;
 PI Thanassi JA;
 DR WPI; 2001-496721/54.
 DR N-PSDB; AAH90731.
 XX
 PT Nucleic acids encoding conserved essential genes involved in bacterial
 PT replication which are potential targets for the treatment of antibiotic
 PT resistant bacterial infections -
 XX
 PS Claim 27; Page 273; 380pp; English.
 XX
 CC The present invention relates to nucleic acids (AAH90701-AAH90918)
 CC encoding polypeptides (AAM01002-AAM01114), which are essential for the
 CC viability of a bacterial cell wall. The acronym CFE stands for "CEG For
 CC Expression", where CEG stands for "Conserved Essential Gene". The nucleic

XX		Streptococcus pneumoniae.
XX	PX	MM0200044865-A1.
XX	PD	03-AUG-2000.
XX	PF	19-JAN-2000; 2000WO-USO1131.
XX	PR	27-JAN-1999; 99US-0239052.
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.
PI	PI	Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;
PI	PI	Warren RL, Kosmatka AL, McDevitt D, Ingraham KA, Chalkier AF;
DR	N-PSDB:	AAR74684.
PT		WPI: 2000-482971/42.
PT		FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
PT		treat microbial diseases, identify agonists and antagonists for
PT		treating microbial infections and to detect diseases associated with
XX		microbial infections .
PS		Claim 1; Page 3; 40pp; English.
CC		The present sequence is a FabG (2-oxoacyl-acyl carrier protein
CC		reductase) polypeptide. A full length Fabg gene was isolated from a
CC		Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
CC		polynucleotides and polypeptides are used for detection and treatment of
CC		microbial diseases. They may also be used to identify antagonists and
CC		agonists which can then be used to treat microbial diseases. Compounds
CC		that interfere with the initial physical interaction between a pathogen
CC		and a host have been identified. The compounds are able to prevent the
CC		adhesion of bacteria to mammalian extracellular proteins in wounds,
CC		prevent adhesion between mammalian extracellular proteins and bacterial
CC		Fabg proteins which mediate tissue damage and/or to block normal
CC		progression of pathogenesis in infections mediated by implantation of
CC		in-dwelling devices or other surgical techniques. The Fabg
CC		polypeptides, polynucleotides, antagonists and agonists are especially
CC		useful in the treatment of Helicobacter pylori infection. They may be
CC		used to decrease H. pylori-induced cancers and to prevent, inhibit
CC		and/or cure gastric ulcers and gastritis.
XX		
SQ	Sequence	243 AA;
OY	Query Match	25.2%; Score 328.5; DB 21; Length 243;
OY	Best Local Similarity	35.1%; Pred. No. 7.7e-24;
MATCHES	88; Conservative	36; Mismatches 104; Indels 23; Gaps 6;
OY	15 ITGASGIGLTAELVVGAGASAVYLDDLPNSGE-----AQAKTLGNNCVAPADYVE	68
DB	10 ITGSIRGGILAIHKFAQGANIVL----NSRGAISELLAFSTYGIKVPISGDVSDF	65
OY	69 KDVOGTALALARGKFGRVDVAVNACIAVAASKTYNNKKGOTHTLEDFORYLDVNLMGTENV	128
DB	66 ADARKMIDQAIAELTSVDVLVNNAGI--TODITLMKMK-----EADFQEKALKNLGAFNM	119
OY	129 IRIVAGEGUNDPPDGGOGRGVITINASVAFFGOVGOAAYSASKGIYMTLPFIARDLAP	188
DB	120 TQSIVL-----KPMKAREGAILNMSVVYGLMGNIQGANYASKGLIGFTSVAREVAS	173
OY	189 IGIRVMYIAPGIEGTPLLTSLPEKYANFLASCVPSPSRIGDAERYAHNVQAITENPFLNG	248
DB	174 RNIRRVNAVLAEGMIEDMDAILSDKIKEATLQIIPM-KERGGAEOVADLVTFVLGADYLTG	232
OY	249 EYIRUDGAIM 259	
DB	233 CVYIALDGGLSM 243	

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AU37767
ID AU37767 standard; Protein; 243 AA.
XX
AC
XX AU37767:
DT
XX 14-FEB-2002 (first entry)
XX
DE Streptococcus pneumoniae cellular proliferation protein #196.
XX
KW Antisense: prokaryotic cellular proliferation protein;
antibiotic; antibacterial; drug design.
XX
OS Streptococcus pneumoniae.
XX
PN W0200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001MO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
XX
PR 23-MAY-2000; 2000US-206848P.
XX
PR 26-MAY-2000; 2000US-207727P.
XX
PR 23-OCT-2000; 2000US-242578P.
XX
PR 27-NOV-2000; 2000US-253625P.
XX
PR 22-DEC-2000; 2000US-257931P.
XX
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
XX
DR N-PSDB; AASS5626.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
PS Example 3; Seq ID No 1360; 511bp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Bacteriella coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pot_sequences.
XX
SO Sequence 243 AA:

Query Match 25.28; Score 328.5; DB 22; Length 243;
Best Local Similarity 35.14; Pied. No. 7.7e-24;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6

15 ITGASGAGTATERLTVGOGASAVLLDLDPNSGCE-----AOAKKLGNVCYFAPADYTS 68
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 10 ITGSSRRGIGLAIHKRFAOGAGNIVL-----NSGALSEELDLFESNYGKIVPIGSDVSDF 65
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
69 KDVOATALALAKGFRGVADVAVNCAGIATVASKTYLNKKQOTHTLDFQFVLDVNIKGFNV 128
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :

```


XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -

PS Claim 1; Page 3542; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30695) from group B
 CC Streptococcus (Streptococcus agalactiae) or group A Streptococcus (SAS
 CC (Streptococcus pyogenes)), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and anti-inflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6004-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

SO Sequence 243 AA:

Query Match 27.1%; Score 353; DB 23; Length 243;
 Best Local Similarity 35.4%; Pred. No. 3.1e-26;
 Matches 92; Conservative 42; Mismatches 100; Indels 26; Gaps 6;

XX 8 VKGLVAVITGASGLTAEKLVGASAVLLDIPNSGGEAQAAL-----GNNCVF 60
 DB 3 IKNTI-FITGSTRIGLMAHQFASLEANIYL-----NRSALISELVASTFDYVTVT 56

XX 61 AAPDVTSERDVOTALAKGKRGVDVAVNCAGIAVASTYMLKKGQHTLEDPRVLDV 120
 DB 57 ISGDVSEASEAKMVEALIESLSIDVILVNNAGIT-----NDKMLTKYTEDFRVLKI 110

XX 121 NLMTGTVNIRLVAGEGNEPDGQGVYIINTASVAFEGQVQAASASKGIVGML 180
 DB 111 NLGTANMTQSVL-----KPMKAKAGALINSSVYGLTGNIGQANVAAKAGMIGFTK 164

XX 181 PIKDLAPGIRMTAPGLFGPLITSLEPKYANFLASQVPPPSRLGPAEYAHLYQAI 240
 DB 165 SVAREVAARNICVNAAPFIESDMTGVLPEKMQEILISQIPM-KRIGAKQEVAAHLASFL 223

XX 241 IENPFLNGEYIRLDGAIRMQ 260
 DB 224 VEODYITGVYIALDGGMWQ 243

RESULT 8
 AAM80670
 ID AAM80670 standard; Protein; 243 AA.

XX AAM80670:
 DT 24-DEC-1998 (first entry)

XX 5. pneumoniae fatty acid biosynthesis protein.
 XX Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
 KM virulence; antibody; infection; detection; treatment; hypothetical;
 KM cell wall biosynthetic; external target; minimal gene set protein.
 XX Streptococcus pneumoniae.
 OS WO9826072-A1.
 PN 18-JUN-1998.
 XX 09-DEC-1997; 97WO-US22578.

XX 13-DEC-1996; 96US-0036281.
 PR (EHL) LILLY & CO ELI.

XX Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;
 PI Mills BJ, Norris FH, Peery RB, Rockey PK, Rostock PR;
 PI Skatard PJ, Smith MC, Solenberg PJ, Treadway PJ;
 PI Young Bellido ML;
 DR WPI; 1998-348529/30.

XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
 PT for evaluating gene expression, and identification of virulence
 PT genes

PS Claim 3; Page 270; 333pp; English.

XX This sequence represents a S. pneumoniae fatty acid biosynthesis
 CC protein. The invention provides DNA sequences (AAM65201 to AAM65304)
 CC from the Streptococcus pneumoniae genome and corresponding protein
 CC sequences (AAM80605 to AAM80728). The protein sequences are classified as
 CC hypothetical, cell wall biosynthetic, external target, or minimal gene
 CC set proteins. A recombinant host containing a vector comprising any of
 CC the above nucleic acids can be used for the recombinant expression of the
 CC proteins. The invention also provides a DNA chip having arrayed on it at
 CC least 15 base pair fragment of any one or more of these DNA sequences.
 CC The DNA chip can be used methods for evaluating gene expression in S.
 CC pneumoniae and for identifying virulence genes in S. pneumoniae.
 CC Antibodies that selectively bind to the above proteins or peptide
 CC fragments can be used to treat S. pneumoniae infection. The antibodies
 CC can also be used to detect S. pneumoniae cells.

SO Sequence 243 AA:

Query Match 25.2%; Score 328.5; DB 19; Length 243;
 Best Local Similarity 35.1%; Pred. No. 7.7e-24;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

XX 15 ITGSGASGLTAEKLVGASAVLLDIPNSGGE-----AQAKLGNMCFAPADVTSE 68
 DB 10 ITGSSRGIGLAIKFKNAQGANIYL-----NRSALISELVASTFDYVTVT 56

XX 69 KDVTALALAKGKRGVDVAVNCAGIAVASTYMLKKGQHTLEDPRVLDVNLMTGFNV 128
 DB 66 ADARKMIDQALAEIGSVYVILVNNAGI--TQDTMLKM---TEADFEKVLKVNLTGAENM 119

XX 129 IRLVAGEGNEPDGQGVYIINTASVAFEGQVQAASASKGIVGMLPIAPDLAP 188
 DB 120 TQSVL-----KPMKAKAGALINSSVYGLTGNIGQANVAAKAGMIGFTKSVAREVAS 173

XX 189 IGIRVMTAPGLFGPLITSLEPKYANFLASQVPPPSRLGPAEYAHLYQAIENPFLNG 248
 DB 174 ENIRVNTAPGMIESDMTALISDKIKENTLAQIPM-KEFGAQEADVADLVFLAGQDYLTVG 232

XX 249 EVIRLDGAIRMQ 259
 DB 233 QYIAIDGSLM 243

RESULT 9
 AAB15706
 ID AAB15706 standard; Protein; 243 AA.

XX AAB15706:
 DT 07-DEC-2000 (first entry)

XX Streptococcus pneumoniae FabG polypeptide.
 XX Streptococcus pneumoniae; FabG; 3-oxoacyl-acyl carrier protein reductase;
 KM antibacterial; cytostatic; antitumor; cancer; gastric ulcer; gastritis;
 KM Helicobacter pylori infection; microbial infection.

Query Match 51.1%; Score 666.5; DB 18; Length 388;
 Best Local Similarity 53.5%; Pred. No. 1,5e-56;
 Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VGLAVITGGASGLTAERLVGASAVLLDIPNSGGEAQAARKLGNNCFAPADVTSE 67
 DB 143 IEGRFVYTGASAGSAGASARLTAAGAKVIALD-----AEPDAEGAVHAADVTID 196
 QY 68 EKDVTALALAKGKGRVDVAVNCAGIYASRTYLLKKGQHTLEDFOFVIDVIMGFEN 127
 DB 197 ATAQTALATLADRFGRDLGVNCAGIAPAEEM--LGRDGHGIDSFARAVTINLIGSFN 254
 QY 128 VRLVAGEGONGEPDGGQGVIIINTASVAAFEGOVGAAYASAKSGIVGMLPIARDLA 187
 DB 255 MRLAEMAMARNEPVR-GERGVYNTASTIAADQIGVAYATAASKAGVAGMTLPARDLA 313
 QY 188 PIGIRVMTIAPGLFETPLITSLEPKVANFLASQVFPSPRLDPAEYAHLYOAITENPPLN 247
 DB 314 RGIIRVMTIAPGIFETPLILEGLPDQVODSLGAAYFPSPRLGEPSEYALLHHIILANPMLN 373
 QY 248 GEVIRLDGAIKMP 261
 DB 374 GEVIRLDGALRMAP 387

RESULT 6
 ABP28011
 ID ABP28011 standard; Protein: 244 AA.
 XX
 AC ABP28011;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Streptococcus polypeptide SEQ ID NO 5198.
 XX
 KM Streptococcus: GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus agalactiae.
 XX
 PN MO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI: 2002-352536/38.
 DR N-PSDB: ABN68642.

New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -

Claim 1: page 3863; 4525pp; English.

CC The invention relates to a protein (ABP25413-ABP30895) from group B Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.

Sequence 244 AA;

QY 15 ITGGASGLGATLATERLVGASAVLLDIPNSGB-----AQARKLGNNCFAPADVTSE 68
 DB 10 ITGSSRGIGLAIHQFQALGANIVL-----NGRSPISDDLAEFADYGVKVIATSGVSSP 65
 QY 69 KDVOFTALALAKGKGRVDVAVNCAGIYASRTYLLKKGQHTLEDFOFVIDVIMGFENY 128
 DB 66 EDANRMTKEATLASIGSDVAVNNAGIT-----NDKMLTKMTVEDEFSVLIKINLTGAFFM 119
 QY 129 IRLVAGEGONGEPDGGQGVIIINTASVAAFEGOVGAAYASAKSGIVGMLPIARDLA 188
 DB 120 TQSVL-----KPMTKARQGAIIINISSVGLTGVGQANVAASKAGIGFTKSVAREVA 173
 QY 189 IGIIRVMTIAPGLFETPLITSLEPKVANFLASQVFPSPRLDPAEYAHLYOAITENPPLN 248
 DB 174 RGIIRVMTIAPGLFETPLITSLEPKVANFLASQVFPSPRLDPAEYAHLYOAITENPPLN 232
 QY 249 EVIRLDGAIKMP 260
 DB 233 QVIALDGGMTMQ 244

RESULT 7
 ABP27345
 ID ABP27345 standard; Protein: 243 AA.
 XX
 AC ABP27345;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Streptococcus polypeptide SEQ ID NO 3866.
 XX
 KM Streptococcus: GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI: 2002-352536/38.
 DR N-PSDB: ABN67976.

CC (see AAX00611 for described uses).

XX Sequence 227 AA;

Query Match 87.2%; Score 1137; DB 20; Length 227;
 Best Local Similarity 99.6%; Pred. No. 8.1e-103;
 Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 ASAYLLDLPNSGGEGQAARKLGNCCVFAADYTSKDVQATALAKKFGRYDVAVNCAGI 94
 DB 1 ASAYLLDLPNSGGEGQAARKLGNCCVFAADYTSKDVQATALAKKFGRYDVAVNCAGI 60
 QY 95 AVASTYTLKKGGQTHTLEDFOFVLDVNLMTGFNTIRLVAGMGONEDPDGQGRGVIINTA 154
 DB 61 AVASTYTLKKGGQTHTLEDFOFVLDVNLMTGFNTIRLVAGMGONEDPDGQGRGVIINTA 120
 QY 155 SVAAEEGGVGAAYASASKSGIVGMLTPIARDLAPIGIRVMTIAPGLFETPLISLPEKVA 214
 DB 121 SVAAEEGGVGAAYASASKSGIVGMLTPIARDLAPIGIRVMTIAPGLFETPLISLPEKVC 180
 QY 215 NFLASQVPEPSPRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMP 261
 DB 181 NFLASQVPEPSPRLGDPAEYAHVQAIIENPFLNGEVIRLDGAIKMP 227

RESULT 4
 ABB62988
 ID ABB62988 standard; Protein; 255 AA.

XX ABB62988;
 AC
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 15756.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EM;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL07091.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS
 PS Disclosure; SEQ ID NO 15756; 21bp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABLI0176-ABLI30511), expressed DNA
 CC sequences (ABLI01840-ABLI16175) and the encoded proteins
 CC (ABBI7737-ABBI72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIP0
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 255 AA;

Query Match 69.8%; Score 910; DB 22; Length 255;
 Best Local Similarity 68.9%; Pred. No. 1.4e-80;
 Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGLVAVITIGASGLCLATAEPLVGGASAVLLDLPNSGGEGQAARKLGNCCVFAADYTS 67
 DB 2 IKNAVSLTVGGAGGLGRTAERLAKOGASVITLADPSSGNEVAKELGKVFVVDYIS 61
 QY 68 EKDVQATALAKKFGRYDVAVNCAGIAVASKTYTLKKGGQTHTLEDFOFVLDVNLMTGFN 127
 DB 62 EKDVSAALCTAKKFGRLDITVACAGTATAVKTFENKVAARLEDFQFVINITVGFEN 121
 QY 128 VIRLVAGMGONEDPDGQGRGVIINTASVAAEEGGVGAAYASASKSGIVGMLTPIARDLA 187
 DB 122 VIRLSAGLMGANEDPDGQGRGVIINTASVAAEDGIGQAAISAKAAVGMTLPIARDLS 181
 QY 188 PIGIRVMTIAPGLFETPLISLPEKYANFLASQVPEPSPRLGDPAEYAHVQAIIENPFLN 247
 DB 182 TCGIRICTIAPGLFNTPMLAALPEKVRTFLAKSIPPORLGESEYAHVQAIIENPFLN 241
 QY 248 GEVIRLDGAIKMP 261
 DB 242 GEVIRLDGAIKMP 255

RESULT 5
 AAW06513
 ID AAW06513 standard; Protein; 388 AA.

XX AAW06513;
 AC
 XX
 DT 08-MAR-1997 (first entry)
 XX
 DE Flavobacterium ORF-5 gene product.
 XX
 KM Carotenoid; lycopene; beta-carotene; echinenone; canthaxanthin;
 KM zeaxanthin; adonixanthin; astaxanthin.
 XX
 OS Flavobacterium sp. R1534 WT (ATCC 21588).
 XX
 PN EP747483-A2.
 PD 11-DEC-1996.
 PF 29-MAY-1996; 96EP-0108556.
 XX
 PR 09-JUN-1995; 95EP-0108888.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Hohmann H, Pasamontes L, Tessier M, Van Loon A;
 XX
 DR WPI; 1997-023160/03.
 DR N-PSDB; AAT45143.
 XX
 PT Flavobacterium gene sequences encoding carotenoid biosynthesis
 PT enzymes - for the production of carotenoid(s), useful in foods and
 PT animal feeds
 PS
 PS Example 2; Fig 7; 80pp; English.

CC A polypeptide (AAW06513) showing approx. 30% homology to
 CC streptomycete polyketide synthases was identified as the product
 CC of ORF-5 from a carotenoid gene cluster (see also AAT45143) of
 CC Flavobacterium sp. R1534. 5 Other open reading frames of the
 CC gene cluster coded for carotenoid biosynthetic enzymes (see also
 CC AAW06515-18 and AAW00871) and can be used to produce carotenoids in
 CC transformed host cells.

XX Sequence 388 AA;

```

FT      /note="alpha helix region A"
FT      190..196
FT      Region
FT      /note="beta sheet region F"
FT      204..218
FT      Region
FT      /note="alpha helix region F"
FT      247..252
FT      Region
FT      /note="beta sheet region G"
XX      WO954347-A2.
XX      28-OCT-1999.
XX      19-APR-1999; 99WO-EP02610.
XX      17-APR-1998; 98US-0082257.
XX      (HORM-) INST HORMON & FORTPFLANZUNGSFORSCHUNG GM.
XX      Ivell R, Spiess A, Balvers M, Jaehner D, Hansis C;
XX      WPI, 2000-052699/04.
XX      N-PSDB; AA234663.
XX      Novel differential display reverse transcription PCR method used to
XX      detect genes expressed in mutant tissues
XX      Claim 4: Fig 2: 40pp: English.
XX      This sequence represents murine Alzheimer-associated beta-amyloid
XX      binding protein (ERAB, see AY32239), a novel member of the SCAD
XX      (short chain alcohol dehydrogenase) family of steroid metabolising
XX      and related enzymes. The sequence was deduced from cDNA (see
XX      AA234663) identified using a novel differential display RT-PCR method
XX      for analysis of w/wv mouse testis gene products. ERAB is
XX      specifically upregulated in the testicular Leydig cells of w/wv
XX      azoospermic mutant mice, suggesting an important role in the
XX      establishment and support of spermatogenesis. The invention also
XX      relates to vectors, host cells, methods for expressing the ERAB
XX      nucleic acid, and antibodies. The nucleic acid and protein are
XX      useful e.g. as markers for testicular development.
XX      Sequence 260 AA:
XX      Query Match 87.9%; Score 1146; DB 21; Length 260;
XX      Best Local Similarity 87.6%; Pred. No. 1.3e-103;
XX      Matches 226; Conservative 18; Mismatches 14; Indels 0; Gaps 0;
XX      4 ACRSVKGLVAVITGGASGLATATRLVGOGASAVLLDLPNSGGCAOKKLGNNCVFPA 63
XX      3 AVRSYKGLVAVTGGASGLATATRLVGOGATVLLVDPSEGAOKKLGESCIFAPA 62
XX      64 DVTSEKDYQATALAKGKFGRYDVAVNCAGIAVASKTYNLRKGGTHLEDFQVLDVNM 123
XX      63 NVTSEKEIQAAATTLAKKEFGRIDVAVNCAGIAVAKTYHKKKTHLEDFQVAVNMLI 122
XX      124 GFENFIRIVAGMGONEDDGGORGVITNTSVAFPEQVGAAVSASKGIQVMTLPIA 183
XX      123 GFENFIRIVAGMGONEDDGGORGVITNTSVAFPEQVGAAVSASKGIQVMTLPIA 182
XX      184 RDLAFIGIRVMTIAGLFGTPLNLSIPKRVANFLASQVFPFSRLDPAEVAHLVQATIN 243
XX      183 RDLAFIGIRVMTIAGLFGTPLNLSIPKRVANFLASQVFPFSRLDPAEVAHLVQATIN 242
XX      244 PFLNGEVRIRLDGAIKMP 261
XX      243 PFLNGEVRIRLDGAIKMP 260
XX      25-MAR-1999 (first entry)
XX      Fragment of human secreted protein encoded by gene 8.
XX      Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX      diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
XX      developmental abnormality; foetal deficiency; blood; allergy; renal;
XX      immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX      inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX      cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX      osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX      endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX      Homo sapiens.
XX      WO9842738-A1.
XX      01-OCT-1998.
XX      19-MAR-1998; 98WO-US05311.
XX      30-MAY-1997; 97US-0050937.
XX      21-MAR-1997; 97US-0041276.
XX      21-MAR-1997; 97US-0041277.
XX      21-MAR-1997; 97US-0041281.
XX      30-MAY-1997; 97US-0042344.
XX      30-MAY-1997; 97US-0048069.
XX      30-MAY-1997; 97US-0048094.
XX      30-MAY-1997; 97US-0048095.
XX      30-MAY-1997; 97US-0048096.
XX      30-MAY-1997; 97US-0048099.
XX      30-MAY-1997; 97US-0048131.
XX      30-MAY-1997; 97US-0048135.
XX      30-MAY-1997; 97US-0048154.
XX      30-MAY-1997; 97US-0048160.
XX      30-MAY-1997; 97US-0048186.
XX      30-MAY-1997; 97US-0048187.
XX      30-MAY-1997; 97US-0048188.
XX      30-MAY-1997; 97US-0048350.
XX      30-MAY-1997; 97US-0048351.
XX      30-MAY-1997; 97US-0048352.
XX      30-MAY-1997; 97US-0048355.
XX      05-AUG-1997; 97US-0054804.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      Brewer LA, Duan R, Ebner R, Ferrite AM, Florence KA;
XX      Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
XX      Rosen CA, Ruben SM, Shi Y, Young P;
XX      WPI: 1999-070066/06.
XX      N-PSDB; AAX00618.
XX      New isolated human genes and the secreted polypeptides they encode -
XX      useful for diagnosis and treatment of e.g. cancers, neurological
XX      disorders, immune diseases, inflammation or blood disorders
XX      Disclosure; Page 11; 385pp; English.
XX      This sequence represents a fragment of a secreted human protein encoded
XX      by the nucleic acid molecule detailed in the descriptor line. The gene
XX      can be used to generate fusion proteins by linking to the gene to a
XX      human immunoglobulin Fc portion (e.g. AAX00602) for increasing the
XX      stability of the fused protein as compared to the human protein only.
XX      The invention relates to 87 novel genes and their fragments (nucleic
XX      acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
XX      which are useful for preventing, treating or ameliorating medical
XX      conditions e.g. by protein or gene therapy. Also, pathological
XX      conditions can be diagnosed by determining the amount of the new
XX      polypeptides in a sample or by determining the presence of mutations in
XX      the new polynucleotides. Specific uses are described for each of the 87
XX      polynucleotides, based on which tissues they are most highly expressed in

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RESULT 3
 AAW67934
 ID AAW67934 standard; Protein: 227 AA.
 XX
 AC AAW67934;

84 267.5 20.5 246 22 AAE02195 S. aureus NADPH-de
85 267 20.5 261 13 AAR77756 NAD affinity gluc
86 267 20.5 276 23 AAY54416 Secoisolaricresin
87 267 20.5 276 23 AAO21494 Secoisolaricresin
88 266 20.4 247 16 AAR66291 Mycobacterium bovi
89 266 20.4 247 16 AAR63899 M. bovis p55 ORF1
90 266 20.4 247 18 AAR40809 M. bovis p55 opero
91 265.5 20.4 268 22 ABB52552 Escherichia coli p
92 265 20.3 340 21 AAB10740 B. megaterium gluc
93 265 20.3 340 21 AAB10741 H. phillipii/B. me
94 264.5 20.3 252 23 AAO16940 Recombinant enzyme
95 264 20.2 243 23 ABB54107 Lactococcus lactis
96 263 20.2 253 22 AAU36249 Pseudomonas aerugi
97 262.5 20.1 273 22 AAY54414 Secoisolaricresin
98 261 20.0 261 23 AAE20115 Lactobacillus tham
99 261 20.0 277 21 AAY54413 Secoisolaricresin
100 260 19.9 261 9 AAB80590 Sequence of glucos

ALIGNMENTS

RESULT 1
AAW71471
ID AAW71471 standard; Protein; 261 AA.

XX AAW71471;
XX 16-DEC-1998 (first entry)

DE ERAB protein.

XX Endoplasmic reticulum associated amyloid-beta peptide binding protein;
KW ERAB protein; amyloid-beta peptide; inhibitor; demyelinating disease;
KW neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;
KW Down's syndrome; Parkinson's disease; Huntington's disease;
KW multiple sclerosis.

XX Homo sapiens.

XX WO9840484-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US04915.

XX 12-MAR-1997; 97US-0815225.

XX (UYCO) UNIV COLUMBIA NEW YORK.

PI Stern DM, Yan SD;

XX WPI, 1998-531524/45.

DR N-PSDB; AAV60576.

XX Endoplasmic reticulum associated amyloid-beta peptide binding
PT protein - inhibitors of which can be used to treat neurodegenerative
PT disorders

PS Claim 2; Fig 1D; 53pp; English.

XX This sequence is the endoplasmic reticulum associated amyloid-beta
CC peptide binding (ERAB) protein of the invention. The protein can be used
CC in a method for evaluating the ability of an agent to inhibit binding of
CC ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the
CC ERAB polypeptide, the agent and amyloid-beta peptide under binding
CC conditions; (b) determining the amount of amyloid-beta peptide bound to
CC ERAB polypeptide; (c) comparison of the amount of binding with results
CC from a control using no agent, so determining inhibition ability of the
CC agent. The inhibitors identified by the method can be used to treat a
CC neurodegenerative condition by administration of an agent that inhibits
CC binding of an ERAB polypeptide to amyloid-beta peptide, particularly
CC where the disease is Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, Huntington's disease, schizophrenia, a demyelinating disease, or
CC multiple sclerosis. The inhibitors can also be used to treat other
CC neurodegenerative conditions including those associated with ageing,
CC dentatorubral and pallidolysian atrophy, Machado-Joseph disease,
CC muscular dystrophy, senility, spinocerebellar ataxia type I, spinobulbar
CC muscular atrophy, stroke, and trauma.

XX Sequence 261 AA;

Query Match 99.7%; Score 1300; DB 19; Length 261;
Best Local Similarity 99.6%; Pred. No. 1,2e-118;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGLATAEERLYVGAGAVLLDPNSGGEAAKKNVCF 60

DB 1 MAACRSYKGLVAVITGASGLGLATAEERLYVGAGAVLLDPNSGGEAAKKNVCF 60

QY 61 APADVTSKDVQOTALALANGKFGVDVAVNACIAVASTYLUKKQGTHTLDFORVDV 120

DB 61 APADVTSKDVQOTALALANGKFGVDVAVNACIAVASTYLUKKQGTHTLDFORVDV 120

QY 121 NLNGTFVIRLVAGEGONPEPDGOGGVYINTASVAEFGVGAAVASKGIGVMTL 180

DB 121 NLNGTFVIRLVAGEGONPEPDGOGGVYINTASVAEFGVGAAVASKGIGVMTL 180

QY 181 PIARDLAPIGIRVMTIAPGLFGTPLLTSPEKYANFLASOVPPSRKLPAPRYAHVQAI 240

DB 181 PIARDLAPIGIRVMTIAPGLFGTPLLTSPEKYANFLASOVPPSRKLPAPRYAHVQAI 240

QY 241 IENPFLNGEYIRIDGAIIRMQP 261

DB 241 IENPFLNGEYIRIDGAIIRMQP 261

RESULT 2
AA332239
ID AAY32239 standard; Protein; 260 AA.

XX AAY32239;

XX 15-FEB-2000 (first entry)

XX Alzheimer-associated beta-amyloid binding protein (ERAB).

XX Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;

XX Leydig cell; differential display RT-PCR; DDRT-PCR;

XX short chain alcohol dehydrogenase; SCAD; testis; marker;

XX spermatogenesis.

XX Mus musculus.

XX Location/Qualifiers

XX 10..15 /note= "beta sheet region A"

XX 18..32 /note= "alpha helix region A"

XX 35..41 /note= "beta sheet region B"

XX 43..57 /note= "alpha helix region B"

XX 61..66 /note= "beta sheet region C"

XX 70..80 /note= "alpha helix region C"

XX 84..94 /note= "beta sheet region D"

XX 109..133 /note= "alpha helix region D"

XX 143..153 /note= "beta sheet region E"

XX 167..171 /note= "SCAD motif"

XX 165..186

disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (1) affects biorythms or circadian cycles of rhythms, fertility, metabolism, cataplexy, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAU28020-AAU28395 represent novel human secreted protein amino acid sequences of the invention.

XX SQ Sequence 288 AA;

Query Match 23.0%; Score 300.5; DB 22; Length 288;
Best Local Similarity 29.9%; Pred. No. 5.3e-21;
Matches 84; Conservative 44; Mismatches 110; Indels 43; Gaps 6;

OY 1 MAACRSVKGVLAVITIGASGLAIAERLYGGAANVLDPNSGGEAAKRLGNNVF 60
DB 10 MAFGTR-YAGKVAVVTGGRGIGAGIVRAFNAGARVTDKDESGRLDEGLPGCGL 68
OY 61 APADVTSEKDVOTALALAKRFGKRVAVNAGIAVASKTYNKKQTHLEDFORVLDV 120
DB 69 SFQVYEDDVKTIVSTIRFGRIDCVNNAGHPP-----ORPETSAGHGFOLLEL 123
OY 121 NMGTENVIRLVAGEMQNEPDGGGQGVIIINTASVAFAFGVGAASAKSGIGVMTL 180
DB 124 NLGTYTLTKLALPYLRSQ-----GVINISLVLGALGQAQAVPYATKGAIVATMK 176
OY 181 PIADLAPIGIRVITAPGLFGLTSLPEKVCNPLASQVPP-----SRLGDPAEYA 224
DB 177 ALADESPYGRVNCISPGNITWPLME-----LAALMPDRATIRREGMLAQRSGV 228
OY 225 -----SRLGDPAEY-AHLVQAIIENPFLNGEVIRLDGAIRM 259
DB 229 QIQPLGRMGCPAEVGAAYFLASFNCTGIXLVTGAEEL 269

RESULT 24

ABP39667
ID ABP39667 standard; Protein: 263 AA.

XX AC ABP39667;

DE 24-JUL-2002 (first entry)

Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4512.

XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

KW antibacterial; gene therapy.

OS Staphylococcus epidermidis.

XX US6380370-B1.

XX 30-APR-2002.

XX 13-AUG-1998; 98US-0134001.

XX 14-AUG-1997; 97US-055779P.

XX 08-NOV-1997; 97US-064964P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Doucette-Stamm LA, Bush D;

XX WPI; 2002-381255/41.

XX N-PSDB; ABN92212.

XX Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -

PS Disclosure; SEQ ID 4512; 267pp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP3124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences
CC can also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life
CC cycle or inhibit S. epidermidis infection.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site.

XX SQ Sequence 263 AA;

Query Match 22.5%; Score 295; DB 23; Length 263;
Best Local Similarity 32.3%; Pred. No. 1.6e-20;
Matches 86; Conservative 42; Mismatches 104; Indels 34; Gaps 6;

OY 12 VAVITGGASGLIAERLYGGAANVLDPNSGGEAAKRL--GNNCFAPADVTSE 68
DB 11 VAVVGAAGIGLKTAEIRLFEDGYSIALVDREAVAKSAERLSGGEAVAFRADVSNR 70
OY 69 KDVTALALAKRFGKRVAVNAGIAVASKTYNKKQTHLEDFQRYLDVNLGTFNV 128
DB 71 DQVESVLNQVHEHFGDLNVLVNNAGIGPMTPI-----ESVTPQFNQVGVNAGVFWG 124
OY 129 IRLVAGEMQNEPDGGGQGVIIINTASVAFAFGVGAASAKSGIGVMTLPIARDLAP 188
DB 125 IGAALIEQF-----DKLGHGKTIINATSOAGVEGNAGLSYSTKFAVRGLTQVAAARDLAE 179
OY 189 IGIRVITAPGLFGLTSLPEKVCNPLASQVPP-----SRLGDPAEYA 234
DB 180 KNTVAFAPGIIETPMMKGIAXK-----LAENNPQMEWGMQFTDQIALKRLSKPEDEVA 235
OY 235 HLVOAII--ENPFLNGEVIRLDGAIRM 258
DB 236 NVVSFLAGSDSYITGOTIIVDGMR 261

RESULT 25

AA683032
ID AA683032 standard; Protein: 262 AA.

XX AC AA683032;

DE 03-SEP-2001 (first entry)

S. epidermidis open reading frame protein sequence SEQ ID NO:3158.

XX Staphylococcus epidermidis SRI strain; infection; diagnosis;

KW vaccination; endocarditis.

OS Staphylococcus epidermidis.

XX WO200134809-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US30782.

XX 09-NOV-1999; 99US-0164258.

XX (GLAX) GLAXO GROUP LTD.

XX Kimmery WJ;

XX WPI; 2001-316495/33.

XX N-PSDB; AAH53882.

XX Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -

XX 25-OCT-2000 (first entry)

DF Bacillus megaterium 3-keto-acyl-CoA reductase Phab.

DE polyhydroxyalkanoate; polyhydroxybutyrate; transgenic plant; Phab;

XX 3-keto-acyl-CoA reductase.

KM Bacillus megaterium.

OS WO200040730-A1.

PN 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US00364.

PF 07-JAN-1999; 99US-0115592.

XX (UYMA-) UNIV MASSACHUSETTS.

PA Cannon MC, Cannon FC, MCCool GJ, Valentin HE, Gruys KU;

PI WPI: 2000-532624/48.

DR N-PSDB; AAs50142.

XX New nucleic acid fragment encoding proteins involved in

PT polyhydroxyalkanoate (PHA) biosynthesis, useful in the production of

PT transgenic plants or recombinant plant cells which can express PHAs

PT such as polyhydroxybutyrate -

XX Claim 85; page 137-138; 153pp; English.

PS The present sequence is that of Phab, a 3-keto-acyl-CoA-reductase

CC protein of Bacillus megaterium. The sequence was deduced from an

CC open reading frame identified in an isolated 7,916 bp fragment of

CC B. megaterium strain 11561 genomic DNA (see AAs50142). The 7,916 bp

CC DNA fragment includes genes encoding proteins (see AAY95743-47)

CC involved in polyhydroxyalkanoate (PHA) biosynthesis. Nucleic acids

CC encoding these proteins are useful for creating transgenic plants or

CC recombinant host cells which have the capability of expressing PHAs

CC such as polyhydroxybutyrate, polyhydroxyvalerate,

CC polyhydroxyhexanoate, polyhydroxyoctanoate, polyhydroxydecanoate or

CC their copolymers. Claimed methods for preparing a PHA involve

CC obtaining a plant or a cell comprising a nucleic acid encoding

CC a 3-keto-acyl-CoA reductase (especially the present acid sequence), and

CC a nucleic acid encoding a PHA synthase (see AAY95747), and growing

CC the plant or cell under conditions suitable for PHA production.

XX Sequence 247 AA:

SQ

Query Match 23.0%; Score 301; DB 21; Length 247;

Best Local Similarity 29.1%; Pred. No. 3.9e-21;

Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVKGLVAVITGAGAGLGIATRAERLVGCG-----ASAVLDDPNSGGEAQAK 53

DB 3 TLQKVAIVTGTSGSGIGALITRELASNGVYAVVYNSKSESAIVEIINDNGSEA--- 58

QY 54 LGNNCFAPADVTSEKEDVOTALAKGFGHVDVAVACGIAVASKTYNLKK-GQTHLE 112

DB 59 -----IANQADVSIVDQAKHIEFTKAFQGLDILVNNAGI---TRRSFKKGE-----E 106

QY 113 DFQRYLVNMGTFENVTLVAVGEGQNEPDGGRGVYIINTASVAAEEGQVGAAYASAK 172

DB 107 DMKRVIDVNLASVYNTTSALTFHLESE---GGR---VINISSITIGAGGFGOTNYSAAK 160

QY 173 GGIYOMTFIARDLPAGIRFVNTIAPGLFGTPLLTSLEPKVCNLSAQVPPSRIGDPAE 232

DB 161 AGMGLFTSLALELAKGVYVNALCPGFIENEMMAIFEDVRAKIVAKIP-TRRLGHAEE 219

QY 233 YAH-LVQAIENPFLNGEVITLDAQIRM 259

DB 220 IARGVVIYAKDGAAYITGQOLNINGLVM 247

RESULT 23

AAU28296

ID AAU28296 standard; Protein: 288 AA.

XX AAU28296;

AC 18-DEC-2001 (first entry)

XX

DT Novel human secretory protein, Seq ID No 653.

DE Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;

XX Ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;

KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;

KW gut protection; lung; liver fibrosis; immune deficiency; infection;

KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;

KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;

XX fertility; analgesic; pain; antigen.

XX Homo sapiens.

XX MO200166689-A2.

PN 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US04942.

XX 07-MAR-2000; 2000US-0519705.

PR 19-MAY-2000; 2000US-0574454.

PR 17-JUN-2000; 2000US-0596193.

PR 14-JUL-2000; 2000US-0616847.

PR 19-SEP-2000; 2000US-0663563.

PR 20-OCT-2000; 2000US-0693267.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

PI WPI: 2001-589934/66.

DR N-PSDB; AAs5196.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries

PT prepared from various human tissues, for diagnosis and treatment of

PT cancer, neurological, inflammatory, and autoimmune disorders -

XX Example 2; SEQ ID No 653; 107pp; English.

PS The invention relates to novel isolated human secreted polypeptides (I)

XX and polynucleotides (II). (I) and (II) are useful for treating

CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,

CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is

CC involved in increasing haematopoiesis, stem cell survival, bone growth

CC and remodeling. (I), (II) and modulators of (II) are useful for

CC prophylaxis or treatment of one or more cancers. (II) is also useful for

CC creating transgenic animals useful for studying the in vivo activities of

CC the polypeptide as well as for studying modulators of the polypeptides.

CC (I) induces the proliferation of neural cells and regeneration of nerve

CC and brain tissue and is useful for the treatment of central and

CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,

CC Parkinson's disease, Huntington's disease, and amyotrophic lateral

CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic

CC activity, regulation of haematopoiesis and is useful for treating myeloid

CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia

CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve

CC tissue growth, and in tissue repair, healing of burns, incisions,

CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative

CC disorders, or periodontal disease. Furthermore, (I) is also useful for

CC gut protection or regeneration and treatment of lung or liver fibrosis,

CC reperfusion injury in various tissues, various immune deficiencies and

PR 05-APR-1999; 99JP-0098205.
 XX (DAIL) DAICEL CHEM IND LTD.
 XX
 PI Yamamoto H;
 XX
 DR WPI, 2000-118183/11.
 DR N-PSDB; AA245749.
 PT Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -
 XX
 PS Claim 6; Page 19-20; 34pp; English.
 XX
 CC The present sequence represents a beta-ketoacyl-ACP reductase protein
 CC of *Bacillus subtilis*. The beta-ketoacyl-ACP reductase enzyme constitutes
 CC a type II fatty acid synthetase. The enzyme has an extremely high
 CC reducing activity and stereoselectivity towards 4-chloroacetoacetic
 CC acid ester. The specification describes a method for producing a
 CC (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
 CC asymmetrically reducing 4-halo-acetoacetic acid ester or its
 CC derivative with beta-ketoacyl-acyl carrier protein reductase
 CC constituting type II fatty acid synthase, or acetoacetyl-coA
 CC reductase constituting the polypeptide hydroxy fatty acid biosynthesis
 CC system. The novel method is used to produce optically active
 CC 4-halo-3-hydroxybutyric acid ester, with a high purity.
 CC
 XX
 SQ Sequence 248 AA;
 Query Match 23.7%; Score 310.5; DB 21; Length 248;
 Best Local Similarity 29.7%; Pred. No. 4.6e-22;
 Matches 76; Conservative 55; Mismatches 100; Indels 25; Gaps 6;
 OY 13 AVINGASGIGLATAERLVGQASAVLLDLPNSGGEAQA-----KILGNCVFAPADY 65
 DB 9 AIVTASGIRGIRSLALALAKSGANV---VYNSGNEKANEVDEIKSMGRKAIKADY 65
 OY 66 TSEEDVOTALLAKGKGRVDVAVNCAGIVASKTYMLKGCQHTLEDFFQRYLDVIMGT 125
 DB 66 SNPDVONMKIKETLSVFSTIDILVNNAGITRDLIMRMKE-----DEMDDVINIMLKV 119
 OY 126 FNVIRLVAGEGONEPDGQGVITINTASVAAFEQGVQGAASASKSGIVGMLPIARD 185
 DB 120 FNCIKATYROMKQ-----RSGRIIVSSIVGSSGMPGQANVYAAAGVIGLTKSAAKE 173
 OY 186 LAPGIRVMTAPLEGFTPLITSLEPKYCNFLASQVFFPRLDPAIYAHVQAIIEN-- 243
 DB 174 LASNITVYNAIAPGFISTDMTKLAKVDQEMKQIPL-ARFEPDSVSSVTFFLASEGA 232
 OY 244 PFLNGEVRILDGAIKM 259
 DB 233 RYMTGQTLHIDGKVM 248

XX
 PR 11-APR-2000; 2000FR-0004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 PI Dussurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Doman E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madueno E, De Pablos B, Wehlund J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 DR WPI, 2002-010914/01.
 XX
 PT Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
 PT and prevention of *Listeria* and related bacterial infections, and
 PT related polypeptides -
 XX
 PS Claim 6; SEQ ID No 1597; 192pp; French.
 CC The present invention relates to the genome sequence of *Listeria*
 CC monocytogenes Egd-e (see AB403041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in *L.*
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies, identification of *L. monocytogenes* and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccine compositions for the treatment or prevention of infections by *L.*
 CC monocytogenes and related organisms.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at http://wipo.int/pub/published_pcl_sequences.
 CC
 XX
 SQ Sequence 247 AA;
 Query Match 23.2%; Score 303.5; DB 23; Length 247;
 Best Local Similarity 32.0%; Pred. No. 2.2e-21;
 Matches 85; Conservative 45; Mismatches 103; Indels 33; Gaps 7;
 OY 7 SVKGLVAVITGASGIGLATAERLVGQASAVLLDLPNSGGEAQA-----KKL-----GNNC 58
 DB 2 TLQGRVAVVTGSGRIGRIDIAINLAKEGANIRF-----VYNSGPEAAETAKLVABHGEV 57
 OY 59 VFAPADYSEKDVOTALLAKGKGRVDVAVNCAGIVASKTYNKKGCQHTLEDFFQRYL 118
 DB 58 EAKKAVVAIAEDVDAFFKQAIERFGRVDILVNNAGITRDLIMRMKE-----DEMDDVI 111
 OY 119 DVNLGCTFNVIRLVAGEGONEPDGQGVITINTASVAAFEQGVQGAASASKSGIVGM 178
 DB 112 NINLKGTFICTRAVSRFMKQ-----RAGKIINNASVVLGIGNGOANVYASKAGVIGL 165
 OY 179 TLPILARDLAPIGIRVMTAPLEGFTPLITSLEPKYCNFLASQVFFPRLDPAIYAHVQA 238
 DB 166 TKTTAEIAPRGIVNNAVAPGFITDMTKLDEKREMLAQIP-----LGAIGTEDIAN 221
 OY 239 AII-----ENPFLNGEVRILDGAIKM 259
 DB 222 AVFLASDASKYITGOTLSVDGKVM 247

RESULT 22
 AAY95746
 ID AAY95746 standard; Protein; 247 AA.
 XX
 AC AAY95746;

Page 13

PS	Claim 1(a):	Page 83:	95pp:	English.
CC	The present sequence is that of human oxidoreductase OXR-3, as			
CC	deduced from a cDNA clone (see AA8918) isolated from a lung tumour			
CC	cDNA library. The protein shows homology to Escherichia coli			
CC	3-oxoacyl-(acyl)-carrier protein, and includes a short-chain			
CC	dehydrogenase signature. OXR-3 is expressed in nervous, reproductive,			
CC	cardiovascular and gastrointestinal tissue, and may be involved in			
CC	cell proliferation and inflammation. The invention provides OXR-1			
CC	to -8 polypeptides (see AAI9926-33) and polynucleotides (see			
CC	AA8918-59). It also provides methods for using these polypeptides			
CC	and polynucleotides for diagnosing, treating or preventing disorders			
CC	associated with expression of OXR3, especially cell proliferative,			
CC	neurological, genetic, smooth muscle, and autoimmune/inflammatory			
CC	disorders. The proteins can also be used to screen for agonists			
CC	and antagonists useful for treating these conditions, while			
CC	antibodies that bind to OXR3 may be used for diagnosis or in assays			
CC	to monitor patient treatment.			
CC				
SO	Sequence	237 AA:		
XX				
XX	Query Match	23.8%, Score 312, DB 22, Length 237;		
XX	Best Local Similarity	31.6%, Pred. No. 3, 1e-22;		
XX	Matches	80; Conservative 42; Mismatches 105; Indels 26; Gaps 5;		
QY	12 VAVINGGASGGLTAERLVGGASAVLLDLPNSGGGAQAKKLGNNCVFAPADYTSKQV 71			
DB	4 VCAVVGSSRGIGRAVNAQLMARKKRLVAVRNLEGGAKAAAGLDGSDHLAFSCDVAKEHDY 63			
QY	72 QATALAKGKFRGVADVANCAGT----AVASTYVLLKKGQTHLEDFQRLVDVNLKGT 126			
DB	64 QNTFEEMKHLGRVNFVFLVNAAGINRSDLLPRTK-----EDMSQJHTNLLGSM 112			
QY	127 NVIRFLVAGMGQNEPDGGQGRVFINASVAAEFGVGGAQVAAASAKSGVIGKTLPIARDL 186			
DB	113 LCKKAAKMTMQD-----QGGSTVYNGSTVLGKNSGQSYTSASKSGLVGSRRLAKEV 166			
QY	187 APTGRVMTIAPGLFGLPILTLSPKVCNPLASQVPPPSRLDGPAPYAHVLAQATLENPFL 246			
DB	167 AARKKIRVVAVPAFGVHTDMTKLEE--HLKKNPL-GRFGTIEVAHAVALVFLLESPYI 222			
QY	247 NGEVIRLDGAIKM 259			
DB	223 TGHVLYVDGQQL 235			
XX				
XX	RESULT 20			
XX	AAV54422			
XX	ID AAV54422 standard; Protein; 248 AA.			
XX	AAV54422;			
XX	06-APR-2000 (first entry)			
XX				
XX	Amino acid sequence of a beta-ketoacyl-ACP reductase protein.			
XX	Beta-ketoacyl-ACP reductase; Type II fatty acid synthetase;			
XX	stereoselectivity; 4-chloroacetoacetic acid ester;			
XX	(S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;			
XX	beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;			
XX	polybeta-hydroxy fatty acid biosynthesis; optically active;			
XX	4-haol-3-hydroxybutyric acid ester.			
XX				
XX	Bacillus subtilis.			
XX				
XX	EP955375-A2.			
XX	10-NOV-1999.			
XX				
XX	10-MAY-1999: 99EP-0109403.			
XX				
XX	08-MAY-1998: 98JP-0126507.			
XX	21-OCT-1998: 98JP-0300178.			

OS Pyrococcus abyssi.
 XX
 FN FR2792651-A1.
 XX
 PD 27-OCT-2000.
 XX
 PF 21-APR-1999; 99FR-0005034.
 XX
 PR 21-APR-1999; 99FR-0005034.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX (IFRE-) IFREMER INST FR RECH EXPL MER.
 PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
 XX Querellou J, Weissenbach J, Saurin W, Hellig R;
 DR WPI; 2001-126236/14.
 XX
 PT New nucleotide sequences isolated from Pyrococcus abyssi encode
 XX proteins useful in industry.
 PS
 XX Claim 7; Pages 1087-1088; 1657pp; French.
 CC The present invention relates to the genomic sequence of Pyrococcus
 CC abyssi (see AAF66431 and AAF41223-7) and P. abyssi proteins. P. abyssi is
 CC a hyperthermophilic archaeon, which is isolated from deep-sea
 CC hydrothermal vents. The present sequence is one such P. abyssi protein.
 CC The proteins of the present invention have various potential industrial
 CC uses, since the proteins are stable at very high temperatures, some up to
 CC 110 degrees centigrade.
 CC Note: This patent is in the same patent family as WO2000065062, which
 CC contains additional sequences as shown in AAB99132-AAB99143,
 CC AAF5903-AAH5920 and AAG66436.
 XX
 SQ Sequence 241 AA;
 Query Match 23.9%; Score 313.5; DB 22; Length 241;
 Best Local Similarity 35.3%; Pred. No. 2.3e-22;
 Matches 91; Conservative 44; Mismatches 88; Indels 35; Gaps 8;
 QY 8 VKGIIVAVTGGASGIGATATARIYVGASAVILDLPHSGGPAOKKIGNNC-----VF 60
 DB 4 LKGVAVLTGASRGIGRAIAIEIAKRGVAVYINRSN---EEAKKTEELCRQGVETTL 60
 QY 61 APAVTSKEDVOTALALAKGKFGKRVDAVAVNCAGIAVASKTYNKKGGTHLEDFQRLDY 120
 DB 61 VKADVSNREEVREKVKYIDKFGRIIDLINNAGI--LQKT---KDPLEVIDEEDRVISV 115
 QY 121 NLKGTFTVIRLYAEMGNENPDGOGGVIIITFASVAFEGVQAAYSAKSGIVGML 180
 DB 116 NLKCAFVITQGVLRYM-----KKGKIVNINISIKGKGIVGPHYASKGGLIALTF 166
 QY 181 PIARDLAPIGIRVITAPGLFTPLTSLPEKVCNFIASGVPEPSRIGD--PAEYAHLY 237
 DB 167 NLARHLAP-NITLVANAVAPGPDVTMLSEKMKLKL-----SLGDIAPKPEVAHAV 218
 QY 238 QAIENPFLNGEVRIRLDG 255
 DB 219 IFLENDHITGEVIDVNG 236
 RESULT 18
 AAU28156
 ID AAU28156 standard; Protein: 237 AA.
 XX
 AC AAU28156;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secretory protein, Seq ID No 325.
 XX
 KM Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KM tschaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KM gut protection; lung; liver fibrosis; immune deficiency; infection;
 KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KM fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 DR WPI; 2001-589934/66.
 DR N-PSDB; AAS45056.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Example 4; SEQ ID No. 325; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing hematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC propylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions, and
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine immunoprotein to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 XX
 SQ Sequence 237 AA;

	Matches	82; Conservative	42; Mismatches	110; Indels	26; Gaps	5;
QY	5	CRSRKGLVAVITGASGLGIAERIVQGSAYLLDLPNSGGEQAQAKKGNVCYFAPAD	64			
Db	17	CDSEMDKRCVAFEGSGSRGIRAVPAQIMARKGIRLAVIANRDEGAKNAAGDLGGDHLAFSCD	76			
QY	65	VTSEKDVQATALAKKGFEKRYDVAVNCAGI-----AVASKTYNKKGGTHRTLEDFORVYLD	119			
Db	77	VAKHEHDVQNTPEEMEKHLGRVNFVYNAGINRDGLVRFKT-----EDWVSQLH	125			
QY	120	VNLMGTFVILVAGCEMGQNEPDGGQGVILINASVAAPFGQVQQAAYSAKSGIVGWT	179			
QY	126	TNLLGSMITCCAAAMRTIMQ-----QGGSIVNGSIVGLGNSQOVSYSKSGELVGSF	179			
Db	180	LPIARDLAPIGIRVWTIAPGLEFGTPLLTSPEKYCNFLASQVPPPSRLGDPAEYAHVQA	239			
Db	180	RALKAEVARKKIRVAVVAPGFVHTDMKDLKEE--HLKKNIPL-GPFGETIEVAHAVVF	235			
QY	240	IIENPFLNGEYIRLDGATRM	259			
Db	236	LIESPYITGHVYVDGGLQL	255			
RESULT	16					
ID	AAM50255					
AC	AAM50255; standard; Protein; 237 AA.					
XX						
DT	21-JAN-2002 (first entry)					
XX						
DE	Human dehydrogenase 21509.					
KW	Dehydrogenase; human; ovarian cancer; colon cancer; lung cancer;					
KW	liver cancer; metastasis; antitumor; therapy; diagnosis.					
OS	Homo sapiens.					
XX						
XX	Key	Location/Qualifiers				
FT	Domain	3..229				
FT	Region	/note="short-chain alcohol dehydrogenase domain"				
FT		148..158				
FT		/note="short-chain alcohol dehydrogenase family signature"				
FT	Modified-site	114..116				
FT		/note="O-phosphorylated by protein kinase C"				
FT	Modified-site	66..69				
FT		/note="O-phosphorylated by casein kinase II"				
FT	Modified-site	95..98				
FT		/note="O-phosphorylated by casein kinase II"				
FT	Modified-site	9..14				
FT		/note="N-myristoylated"				
FT	Modified-site	38..43				
FT		/note="N-myristoylated"				
FT	Modified-site	110..115				
FT		/note="N-myristoylated"				
FT	Modified-site	128..133				
FT		/note="N-myristoylated"				
FT	Modified-site	134..139				
FT		/note="N-myristoylated"				
FT	Modified-site	153..158				
FT		/note="N-myristoylated"				
XX						
XX	WO200175119-A2.					
XX						
PD	11-OCT-2001.					
XX						
PF	02-APR-2001; 2001WO-US10720.					
XX						
PR	31-MAR-2000; 2000US-193920P.					
XX						
PA	(MILL-) MILLENNIUM PHARM INC.					
XX						

Pt	Meyers RA, Rudolph-Owen LA;
Xx	
Df	WPI: 2001-626438/72.
Df	N-PSDB; AAI70573.
Xx	
Pt	Novel isolated 21509, and 33770 polypeptides belonging to human
Pt	dehydrogenase family members, useful for treating cancer, diabetes,
Pt	atherosclerosis, glomerulonephritis, Crohn's disease, cirrhosis,
Pt	multiple sclerosis -
Xx	
Pt	Claim 1(a); Fig 2; 146pp; English.
Xx	
Cc	The present sequence is that of a novel human dehydrogenase,
Cc	designated 21509. The protein has a significant number of
Cc	structural characteristics in common with members of the
Cc	dehydrogenase/oxaloductase family. Its expression pattern
Cc	suggests a role in tumour development. The invention provides
Cc	21509 and 33770 nucleic acids, antisense molecules, recombinant
Cc	expression vectors, host cells and transgenic animals in which a
Cc	21509 or 33770 gene has been introduced or disrupted. It also
Cc	provides 21509 and 33770 proteins, fusion proteins, antigenic
Cc	peptides and antibodies, and methods for screening for compounds
Cc	that modulate the expression or activity of 21509 or 33770
Cc	polypeptides or nucleic acids. Such modulators are used in methods
Cc	for inhibiting the proliferation or migration, or inducing the
Cc	killing, of 21509- or 33770-expressing cells, especially the
Cc	hyperproliferative and/or metastatic cells of a soft tissue tumour,
Cc	solid tumour or metastatic lesion, especially ovarian cancer, colon
Cc	cancer, lung cancer and liver cancer (claimed). Modulator
Cc	compounds are also used in claimed methods of modulating fatty acid
Cc	biosynthesis or retinoid biosynthesis in a cell. 21509 and 33770
Cc	nucleic acids can also be used to prepare diagnostic probes and in
Cc	gene (including antisense) therapy.
Xx	
SQ	Sequence 237 AA:
	Query Match 24.0%; Score 314; DB 22; Length 237;
	Best Local Similarity 32.0%, Pred. No. 2e-22;
	Matches 81; Conservative 41; Mismatches 105; Indels 26; Gaps 5;
Qy	12 VAVINGGASGLTAERLVAGOGASAVLLDLPNSGGGAQAARKLGNCCYFAADVTSEKDV 71
Dd	1 : : : : : : : : : : : : : :
Qy	4 VCALIGGSRGIRGAVACQLMARKVGLAIITARNLECAKKAAADDLGDDHLAFSCDYAKKHVD 63
Dd	1 : : : : : : : : : : : : : :
Qy	72 QFALLAAGKGRGDVAVNCNGI-----AVASKTYNKLKGQTHTEDEQRVLVDNLMTGF 126
Dd	64 QNTPEEMKRLHGRVFLVNAAGINDSLVTKRT-----EDVVSQLHTLTLDSM 112
Qy	127 NVIRLVAGEMCNEPDGOGRGVIVINTASVAAFEQGVQAAYSASKSIGVGMTLPIARDL 186
Dd	113 LTCKAMPAMIQQ-----QGSIYNVGISVGLKNGSQSYSAKSGLVGFSPRLAKEV 166
Qy	187 APIGRRVTFIPGLFGTPLMLSLPKVCNVFLASQVPFPFSRILDPAEVAHLQATINENPFL 246
Dd	167 ARKRIKRVAVAPGVHYDMTRDKLEE---HLKKNPL-GRGGETIEVAHAAYVFLUESPT 222
Qy	247 NGEVIRLDGAIRM 259
Dd	1 : : : : :
Qy	223 TGHVLYVDGDLQ 235
Dd	1 : : : : :
	RESULT 17
	AAB96397
	AAB96397 standard; Protein; 241 AA.
	AAB96397;
	29-OCT-2001 (first entry)
	Putative P. abyssii dehydrogenase #8.
	Hypertrophophilic archaeon; hypertrophophilic protein.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
 PI Yamamoto RT, Xu HH;
 DR WPI: 2001-611495/70.
 DR N-PSDB; AAS53187.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 PS
 PS Example 3; Seq ID No 10921; 51pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SO Sequence 245 AA;
 Query Match 24.3%; Score 318.5; DB 22; Length 245;
 Best Local Similarity 33.7%; Pred. No. 7.5e-23;
 Matches 84; Conservative 38; Mismatches 108; Indels 19; Gaps 5;
 QY 15 ITGASGLGLATRLVVGOGASAVLTD---LPSNGGEAQAATLGNVCVAPADVASEKO 70
 DB 10 ITGSTRIGRAVALAFKAGKANIVLNGRSRITPEQRREITA--FGKCTISDSIDISFPA 67
 QY 71 VQNALALAKGFGKRVDAVAVACAGIYASAKYTNKKGQTHLEDPQRYLVNMGTEVNR 130
 DB 68 AGEWIOATVVDOLGIDILVNNAGIT-----NKLILRMKEPFNCIDINLGTENMQ 121
 QY 131 LVAGEMGONEPDGGGQGVIIINTASVAFEGVGQAAYASAKGIYGMTPIARDLAPIG 190
 DB 122 QAVRMMKQ-----RGRILLMASVSGLMGNNQANYSKAGVGFTSVAREVAPRG 175
 QY 191 IRVATLAPGLEPGLTSLPEKYNFLASQVPPSRLLGDAEVAHLVQAIINPFLNGEV 250
 DB 176 ITCNALPFGFQIOTEMTVLSKRYKQNNAOPIQT-FGVEDVAAFAIFLAKSPYINGV 234
 QY 251 IRLDQATRM 259
 DB 235 VNVDSGLVM 243
 DB
 RESULT 15
 AAU28344
 ID AAU28344 standard; Protein: 257 AA.
 XX
 AC AAU28344;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secretory protein, Seq ID No 701.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 OS Homo sapiens.
 PN WO200166689-A2.
 XX
 XX 13-SEP-2001.
 XX
 PF 05-MAR-2001; 201WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Tang YF, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 DR WPI: 2001-589934/66.
 DR N-PSDB; AAS45244.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 PS
 PS Example 2; SEQ ID No 701; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 XX
 SO Sequence 257 AA;
 Query Match 24.2%; Score 317; DB 22; Length 257;
 Best Local Similarity 31.5%; Pred. No. 1.1e-22;

XX Streptococcus pneumoniae.
OS
XX WO200044885-A1.
FN
XX 03-AUG-2000.
PD
XX 19-JAN-2000; 2000WO-US01131.
PE
XX 27-JAN-1999; 99US-0239052.
PR
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA
XX Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;
PI Warren RL, Kosmatka AL, McDevitt D, Ingraham KA, Chalker AF;
PI So CY, Wallis NG, Pearson SC;
XX
XX WPI: 2000-482971/42.
DR N-PSDB; AAA74684.
DR
XX FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
PT treat microbial diseases, identify agonists and antagonists for
PT treating microbial infections and to detect diseases associated with
PT microbial infections -
XX
XX Claim 1; Page 3; 40pp; English.
XX
XX The present sequence is a FabG (2-oxoacyl-acyl carrier protein
CC reductase) polypeptide. A full length fabg gene was isolated from a
CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
CC polynucleotides and polypeptides are used for detection and treatment of
CC microbial diseases. They may also be used to identify antagonists and
CC agonists which can then be used to treat microbial diseases. Compounds
CC that interfere with the initial physical interaction between a pathogen
CC and a host have been identified. The compounds are able to prevent the
CC adhesion of bacteria to mammalian extracellular proteins in wounds,
CC prevent adhesion between mammalian extracellular proteins and bacterial
CC FabG proteins which mediate tissue damage and/or to block normal
CC progression of pathogenesis in infections mediated by implantation of
CC in-dwelling devices or other surgical techniques. The FabG
CC polypeptides, polynucleotides, antagonists and agonists are especially
CC useful in the treatment of Helicobacter pylori infection. They may be
CC used to decrease H. pylori-induced cancers and to prevent, inhibit
CC and/or cure gastric ulcers and gastritis.
XX
XX Sequence 243 AA:
SQ
Query Match 24.9%; Score 326.5; DB 21; Length 243;
Best Local Similarity 35.1%; Pred. No. 1.2e-23;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
QY 15 ITGASGSLGATATRLVAGGASAVLIDPNSGGE-----AQAKKGNKCFAPADVTSE 68
DB 10 ITGSSRGIGLAIHKEFAQAGANTVL---NSRGAISEELAEFSNYGIRKVPISGVSDF 65
QY 69 KDVOATALAKGTRGVADVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLGTFNV 128
DB 66 ADARIMIDQALAEISGVADVAVNNNGI--TQDTLMKMK---TEADFEVLKVNLTGAFFNM 119
QY 129 IRLVAGGEGNEPDGOGGORYINTASVAAFEQGVGAISAGSGVIGMTLPFARDIAP 188
DB 120 TQSVL-----KPMKAREGAIINNSVVGINGINGANVYASAGLIGFTKSVAREVAA 173
QY 189 IGRMTIAPGLGFTPLTSLPEKVCNPLASQVFPSPSLGDPAEVAHLVQAIINPPLNG 248
DB 174 KNIRNVNAPGMIBEDMALLSDRKIKETLNAQIRM-KRFGQAEVADLTVELAQDVIYTG 232
QY 249 EYIRLDGAI RM 259
DB 233 QVIAIDGGISM 243
RESULT 10

AAU37767
ID AAU37767 standard; Protein; 243 AA.
XX
XX AAU37767;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Streptococcus pneumoniae cellular proliferation protein #196.
DE
XX
XX Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
XX Streptococcus pneumoniae.
OS
XX
XX WO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US09180.
PE
XX
XX 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX
XX Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu H;
PI
XX
XX WPI: 2001-611495/70.
DR N-PSDB; AAS55626.
DR
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PT
XX
XX Example 3; Seq ID No 13360; 511pp; English.
PS
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 243 AA:
Query Match 24.9%; Score 326.5; DB 22; Length 243;
Best Local Similarity 35.1%; Pred. No. 1.2e-23;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
QY 15 ITGASGSLGATATRLVAGGASAVLIDPNSGGE-----AQAKKGNKCFAPADVTSE 68
DB 10 ITGSSRGIGLAIHKEFAQAGANTVL---NSRGAISEELAEFSNYGIRKVPISGVSDF 65
QY 69 KDVOATALAKGTRGVADVAVNCAGIAVASKTYNLKKGQTHLEDFORVLDVNLGTFNV 128

XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 XX
 PS Claim 1; Page 3542; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus (SBS (Streptococcus agalactiae) or group A Streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
 CC the specification. The proteins have antibacterial and anti-inflammatory
 CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
 CC antibodies that bind (1) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a
 CC biological sample. (1) is used to determine whether a compound binds to
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (1) may be used to recombinantly produce (1) and may be
 CC used in gene therapy. Antibodies to (1) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 CC
 SQ Sequence 243 AA;
 Query Match 26.8%; Score 351; DB 23; Length 243;
 Best Local Similarity 35.4%; Pred. No. 5e-26;
 Matches 92; Conservative 42; Mismatches 100; Indels 26; Gaps 6;
 QY 8 VKGIIVITGASGLTAERLVGGASAVLLDLPNSGGEAOKL-----GNNCYF 60
 DB 3 IKGNI-FITGSTRIGIAMAHGFASLEANIYL-----NGRSATSEELVAFSTDYGVTVY 56
 QY 61 APADVSEKDVOTATLAKGKFGVDVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDV 120
 DB 57 ISGVSSASEKRRVNAISLSIDVYNNAGIT-----NDKLMKMTEDPFRVYK 110
 QY 121 NLMGTENVIRLVAGEMGONPDGQGRVITNTASVAEFQVGAAYSAKSGIVGMTL 180
 DB 111 NLTAFAFMTQSVL-----KPMIKARQALINSSVYGLTGNIGQANYAASKAGMIGFTK 164
 QY 181 PIADLDPIGRVMTAPGLFETPLTSLPEKCNFLASOVPPSRGDAEFAHLYQAI 240
 DB 165 SVAREVARNICVNAIPGFTESDMTGVLPKMQEJLSQIPM-KRIGKQEVAAHLASFL 223
 QY 241 IENPFLNGEVIRLDGAI RMQ 260
 DB 224 VEDDYITGVYAIADGGM TMQ 243
 RESULT 8
 AAM80670 ID AAM80670 standard; Protein; 243 AA.
 XX AAM80670;
 AC AAM80670;
 XX 24-DEC-1998 (first entry)
 DE S. pneumoniae fatty acid biosynthesis protein.
 DE Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
 KM virulence; antibody; infection; detection; treatment; hypothetical;
 KM cell wall biosynthetic; external target; minimal gene set protein.
 XX Streptococcus pneumoniae.
 CS Streptococcus pneumoniae.
 XX WO9826072-A1.
 FN 18-JUN-1998.
 XX 09-DEC-1997; 97WO-US22578.
 PF

XX 13-DEC-1996; 96US-0036281.
 PR (ELIT) LILLY & CO ELI.
 XX
 PA Balz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;
 PI Mills BJ, Norris FH, Peery RB, Rokey PK, Rostreck PR;
 PI Skarud PL, Smith MC, Solenberg PT, Treadway PJ;
 PI Young Bellido ML;
 DR WPI; 1998-348529/30.
 XX
 PT Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
 PT for evaluating gene expression, and identification of virulence
 PT genes
 XX
 PS Claim 3; Page 270; 333pp; English.
 XX
 CC This sequence represents a S. pneumoniae fatty acid biosynthesis
 CC protein. The invention provides DNA sequences (AAV65201 to AAV65304)
 CC from the Streptococcus pneumoniae genome and corresponding protein
 CC sequences (AAM80605 to AAM80728). The protein sequences are classified as
 CC hypothetical, cell wall biosynthetic, external target, or minimal gene
 CC set proteins. A recombinant host containing a vector comprising any of
 CC the above nucleic acids can be used for the recombinant expression of the
 CC proteins. The invention also provides a DNA chip having arrayed on it at
 CC least 15 base pair fragment of any one or more of these DNA sequences.
 CC The DNA chip can be used methods for evaluating gene expression in S.
 CC pneumoniae and for identifying virulence genes in S. pneumoniae.
 CC Antibodies that selectively bind to the above proteins or peptide
 CC fragments can be used to detect S. pneumoniae infection. The antibodies
 CC can also be used to detect S. pneumoniae cells.
 CC
 SQ Sequence 243 AA;
 Query Match 24.9%; Score 326.5; DB 19; Length 243;
 Best Local Similarity 35.1%; Pred. No. 1.2e-23;
 Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
 QY 15 ITGASGICLATAEIRLVGGASAVLLDLPNSGGE-----AOKLGNCCYFAPADTVSE 68
 DB 10 ITGSSGICDIAFNHFAQAGANIVL-----NSGATSEELAEFSNYGIRVYPIGSDVDF 65
 QY 69 KDVOTATLAKGKFGVDVAVNCAGIAVASKTYNKKQGTHTLEDFORVLDVNLGTFENV 128
 DB 66 ADAKRVIDDAIHELSDVYVNNAGI--TQDILMKM-----TEADFEVLYKNVLGARNM 119
 QY 129 IRLVAGEMGONPDGQGRVITNTASVAEFQVGAAYSAKSGIVGMTLPIARDIAP 188
 DB 120 TQSVL-----KPMKARREGALINSSVYGLTGNIGQANYAASKAGLIGFTKSAVREVAS 173
 QY 189 IGIRVMTAPGLFETPLTSLPEKCNFLASOVPPSRGDAEFAHLYQAI IENPFLNG 248
 DB 174 RNIRVAVIAPGMIRESMTAILSDRIKATLQIIPM-KEFGQAEQVADLTVPFLAGDYITLG 232
 QY 249 EVIRLDGAI RM 259
 DB 233 QVYAIADGGLSM 243
 RESULT 9
 AAB15706 ID AAB15706 standard; Protein; 243 AA.
 XX AAB15706;
 AC AAB15706;
 XX 07-DEC-2000 (first entry)
 DE Streptococcus pneumoniae Fabg polypeptide.
 DE Streptococcus pneumoniae; Fabg; 3-oxoacyl-acyl carrier protein reductase;
 KM antibacterial; cytosolic; antitumor; cancer; gastric ulcer; gastritis;
 KM Helicobacter pylori infection; microbial infection.

Query Match 50.8%; Score 664.5; DB 18; Length 388;
 Best Local Similarity 55.5%; Pred. No. 2,36-56;
 Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGGASGLGATLAEKLVGGASAVLLDLPNSGGEACAKKIGNNCFAPADYTS 67
 DB 143 IEGHVFVVTGASGLGASAVLLDLPNSGGEACAKKIGNNCFAPADYTS 196
 QY 68 EKDVTALATLAKGFRVDVAVNCAGIAVASKTYNKKGQTHLEDFQRYLDVNLMTGFN 127
 DB 197 ATAGOTATLALTDGFRGLDGLVNCAGIAVASKTYNKKGQTHLEDFQRYLDVNLMTGFN 254
 QY 128 VIRLVAGEMGONEPDGQSGVITNTASVAAFEGQVQAAYSASKGIIVGNTPIARDLA 187
 DB 255 MARLAEMARNEPVR-GERGVIVNTASIAADQIGQVAYVASKAGVAGTILPMARDLA 313
 QY 188 PIGIRVMTIAPGLTPTLTLSPKVCNFLASQVFPFSLRGDPAEVAHLVQATIEENFELN 247
 DB 314 RHGIRVMTIAPGIRTPLEBGLPDQVDSLGAAVFPFSLRGDPAEVAHLVQATIEENFELN 373
 QY 248 GEVIRLDGATIMQ 261
 DB 374 GEVIRLDGATIMQ 387

RESULT 6
 APP28011
 ID APP28011 standard; Protein: 244 AA.
 AC APP28011;
 XX 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 5198.
 XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
 OS Streptococcus agalactiae.
 XX WO200234771-A2.
 XX 02-MAY-2002.
 PD 29-OCT-2001; 2001WO-GB04789.
 PF 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX WPI; 2002-352536/38.
 DR N-PSDB; ABN68642.
 XX New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PI for detecting a compound that binds to the protein -
 XX Claim 1; Page 3863; 4525pp; English.
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.

Sequence 244 AA:
 Query Match 27.6%; Score 361.5; DB 23; Length 244;
 Best Local Similarity 36.5%; Pred. No. 4,76-27;
 Matches 92; Conservative 38; Mismatches 99; Indels 23; Gaps 5;

QY 15 ITGASGLGATLAEKLVGGASAVLLDLPNSGGE-----AQAKKIGNNCFAPADYTS 68
 DB 10 ITGSSRGIGLAIHQFQJGANTVL-----NGRSEISEDIIEADYGVKVIISGVSSF 65
 QY 69 KDVTALATLAKGFRVDVAVNCAGIAVASKTYNKKGQTHLEDFQRYLDVNLMTGFN 128
 DB 66 EDANRMKEALIASLGSVDVLYNNAGIT-----NDKLMKMYDEPESYLKINTLGAFFM 119
 QY 129 IRLVAGEMGONEPDGQSGVITNTASVAAFEGQVQAAYSASKGIIVGNTPIARDLP 188
 DB 120 TQSVL-----KMTKARQGAIIINISSVGLTGNVQAVYASKAGLIGFTSVAREVA 173
 QY 189 IGIRVMTIAPGLTPTLTLSPKVCNFLASQVFPFSLRGDPAEVAHLVQATIEENFELN 248
 DB 174 RGIRVMTIAPGLTPTLTLSPKVCNFLASQVFPFSLRGDPAEVAHLVQATIEENFELN 232
 QY 249 EVIRLDGATIMQ 260
 DB 233 QVIAIDGGMQ 244

RESULT 7
 APP27345
 ID APP27345 standard; Protein: 243 AA.
 AC APP27345;
 XX 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 3866.
 XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX Streptococcus pyogenes.
 XX WO200234771-A2.
 XX 02-MAY-2002.
 PD 29-OCT-2001; 2001WO-GB04789.
 PF 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tettelin H;
 XX WPI; 2002-352536/38.
 DR N-PSDB; ABN67976.

Query Match 87.4%; Score 1144; DB 21; Length 260;
 Best Local Similarity 87.6%; Pred. No. 2.2e-103;
 Matches 226; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 4 ACRSVGLAVITGASGLGATLAEKLVGOGASAVLLDLPNSGGAQAKKIGNNCYFAPADVS 63
 DB 3 AVRSKGLVAVITGASGLGATLAEKLVGOGATVAVLDPNSGGAQAKKIGESCIFAPA 62
 QY 64 DVTSEKDVQATLALAKKFGFVDVAVNCAGIYAVASKTYNLRKQGTHTLEDFQRYLDVNL 123
 DB 63 NVTSEKEIQALTLAKKFGFVDVAVNCAGIYAVASKTYNLRKQGTHTLEDFQRYLDVNL 122
 QY 124 GFENVIRLVAGEMGQNEPDGQGRGVITINTASVAAFEGQVQAAVSASKGIYGMTLPRIA 183
 DB 123 GFENVIRLVAGEMGQNEPDGQGRGVITINTASVAAFEGQVQAAVSASKGIYGMTLPRIA 182
 QY 184 RDLAFIGIRVMTIAPGLFGLTSLPEKVCNFIASQVFPSPRLGDPAEYAHVQALTEEN 243
 DB 183 RDLAFIGIRVMTIAPGLFGLTSLPEKVCNFIASQVFPSPRLGDPAEYAHVQALTEEN 242
 QY 244 PFLNGEVIRLDGAIKMP 261
 DB 243 PFLNGEVIRLDGAIKMP 260

RESULT 4

ABR62988 standard; Protein; 255 AA.

ID ABR62988 standard; Protein; 255 AA.
 AC ABR62988;
 DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SEQ ID NO 15756.
 DE Drosophila melanogaster polypeptide SEQ ID NO 15756.
 KM Drosophila melanogaster polypeptide; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 XX 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR N-PSDB; ABL07091.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT Disclosure; SEQ ID NO 15756; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB57737-AB872072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 255 AA;
 SQ

Query Match 69.4%; Score 908; DB 22; Length 255;
 Best Local Similarity 68.9%; Pred. No. 2.3e-80;
 Matches 175; Conservative 29; Mismatches 50; Indels 0; Gaps 0;

QY 8 VKGIVAVITGASGLGATLAEKLVGOGASAVLLDLPNSGGAQAKKIGNNCYFAPADVS 67
 DB 2 IKNAVSVITGASGLGATLAEKLVGOGASAVLLDLPNSGGAQAKKIGESCIFAPA 61
 QY 68 EKDVOQTALAKKFGFVDVAVNCAGIYAVASKTYNLRKQGTHTLEDFQRYLDVNLGTE 127
 DB 62 EKDVSALQTAQKFGFGLDVTNACAGTAAVKTFFNKNVAHRLDEDFQRYLDVNLGTE 121
 QY 128 VIRLVAGEMGQNEPDGQGRGVITINTASVAAFEGQVQAAVSASKGIYGMTLPRIA 187
 DB 122 VIRLVAGEMGQNEPDGQGRGVITINTASVAAFEGQVQAAVSASKGIYGMTLPRIA 181
 QY 188 PIGIRVMTIAPGLFGLTSLPEKVCNFIASQVFPSPRLGDPAEYAHVQALTEEN 247
 DB 182 TQIRICTIAPGLFGLTSLPEKVCNFIASQVFPSPRLGDPAEYAHVQALTEEN 241
 QY 248 GEVIRLDGAIKMP 261
 DB 242 GEVIRLDGAIKMP 255

RESULT 5

AAW06513 standard; Protein; 388 AA.

ID AAW06513 standard; Protein; 388 AA.
 AC AAW06513;
 DT 08-MAR-1997 (first entry)
 XX Flavobacterium ORF-5 gene product.
 DE Flavobacterium ORF-5 gene product.
 KM Carotenoid; lycopene; beta-carotene; echinenone; canthaxanthin;
 KW zeaxanthin; adonixanthin; astaxanthin.
 OS Flavobacterium sp. R1534 WT (ATCC 21586).
 XX EP747483-A2.
 XX 11-DEC-1996.
 XX 29-MAY-1996; 96EP-0108556.
 XX 09-JUN-1995; 95EP-0108888.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA Hohmann H, Pasamontes L, Tessier M, Van Loon A;
 PI WPI; 1997-023160/03.
 DR N-PSDB; AAT45143.
 XX Flavobacterium gene sequences encoding carotenoid biosynthesis
 PT enzymes - for the production of carotenoid(s), useful in foods and
 PT animal feeds
 PT Example 2; Fig 7; 80pp; English.
 PS A polypeptide (AAW06513) showing approx. 30% homology to
 CC streptomycete polypeptide synthases was identified as the product
 CC of ORF-5 from a carotenoid gene cluster (see also AAT45143) of
 CC Flavobacterium sp. R1534. 5 Other open reading frames of the
 CC gene cluster coded for carotenoid biosynthetic enzymes (see also
 CC AAW06515-18 and AAW00871) and can be used to produce carotenoids in
 CC transformed host cells.
 XX Sequence 388 AA;
 SQ

Query	Subject	Score	Length	Mismatches	Indels	Gaps
QY 35	ASAVLDDLPSNGGEOAKKLGNNCFAPADVTSEKDVOTALALAKGFRGVDAVNCAGI	87.5%	227	0	0	0
DB 1	ASAVLDDLPSNGGEOAKKLGNNCFAPADVTSEKDVOTALALAKGFRGVDAVNCAGI	87.5%	227	0	0	0
QY 95	AVASRTYLNKKGGCHTLEDFPRVLDVNLMTGFNTYRLVAGMGONEPDGGGRGVIINTA	87.5%	227	0	0	0
DB 1	AVASRTYLNKKGGCHTLEDFPRVLDVNLMTGFNTYRLVAGMGONEPDGGGRGVIINTA	87.5%	227	0	0	0
QY 155	SVAFEEQVGGAAVSASKGGIVGNTLPIARDLAPIGIRVMTIADGLSTPLITSPEKVC	87.5%	227	0	0	0
DB 121	SVAFEEQVGGAAVSASKGGIVGNTLPIARDLAPIGIRVMTIADGLSTPLITSPEKVC	87.5%	227	0	0	0
QY 215	NFLASQVFPFSPRLDPAEYAHLYVAATINPFLNGEVIILDAIRNCP	87.5%	227	0	0	0
DB 181	NFLASQVFPFSPRLDPAEYAHLYVAATINPFLNGEVIILDAIRNCP	87.5%	227	0	0	0

XX		Alzheimer-associated beta-amyloid binding protein; ERAB; mouse;
KW	Leydig cell; differential display RT-PCR; DDRT-PCR;	
KM	short chain alcohol dehydrogenase; SCAD; testis; marker;	
XN	spermatogenesis.	
OS	Mus musculus.	
XX		
FH	Key	
FT	Region	
FT	/note= "beta sheet region A"	
FT	18..32	
FT	/note= "alpha helix region A"	
FT	35..41	
FT	/note= "beta sheet region B"	
FT	43..57	
FT	/note= "alpha helix region B"	
FT	61..66	
FT	/note= "beta sheet region C"	
FT	70..80	
FT	/note= "alpha helix region C"	
FT	84..94	
FT	/note= "beta sheet region D"	
FT	109..133	
FT	/note= "alpha helix region D"	
FT	143..153	
FT	/note= "beta sheet region E"	
FT	167..171	
FT	/note= "SCAD motif"	
FT	165..186	
FT	/note= "alpha helix region A"	
FT	190..196	
FT	/note= "beta sheet region F"	
FT	204..218	
FT	/note= "alpha helix region F"	
FT	247..252	
FT	/note= "beta sheet region G"	
XX		
PN	WO954347-A2.	
XX		
PD	28-OCT-1999.	
XX		
PF	19-APR-1999; 99WC-EP02610.	
XX		
PR	17-APR-1998; 98US-0082257.	
XX		
PA	(HORM-) INST HORMON & FORPFLANZUNGSFORSCHUNG GM.	
PI	Ivell R, Splies A, Balvers M, Jaehner D, Hansis C;	
DR	WPI; 2000-052699/04.	
DR	N-PSDB; AA234663.	
XX		
PT	Novel differential display reverse transcription PCR method used to	
PT	detect genes expressed in mutant tissues	
XX		
PS	Claim 4; Fig 2; 4opp; English.	
XX		
CC	This sequence represents murine Alzheimer-associated beta-amyloid	
CC	binding protein (ERAB, see AY332239), a novel member of the SCAD	
CC	(short chain alcohol dehydrogenase) family of steroid metabolising	
CC	and related enzymes. The sequence was deduced from cDNA (see	
CC	AA234663) identified using a novel differential display RT-PCR method	
CC	for analysis of w/wy mouse testis gene products. ERAB is	
CC	specifically upregulated in the testicular Leydig cells of w/wy	
CC	aacospemic mutant mice, suggesting an important role in the	
CC	establishment and support of spermatogenesis. The invention also	
CC	relates to vectors, host cells, methods for expressing the ERAB	
CC	nucleic acid, and antibodies. The nucleic acid and protein are	
CC	useful e.g. as markers for testicular development.	
Sequence	260 AA;	
70		

84	265.5	20.3	246	22	AAE02195	S. aureus NADPH-de
85	265.5	20.3	268	22	AB852552	Escherichia coli p
86	264	20.2	247	16	AA862291	Mycobacterium bovis
87	264	20.2	247	16	AA838899	M. bovis p55 ORF1
88	264	20.2	247	18	AA40809	M. bovis p55 opero
89	264	20.2	276	21	AA54446	Secoisolaricresin
90	264	20.2	276	23	AA021494	Secoisolaricresin
91	263	20.1	261	13	AA827756	NAD affinity glucos
92	262.5	20.1	252	23	AA016940	Recombinant enzyme
93	261	19.9	277	21	AA810740	B. megaterium gluc
94	261	19.9	272	21	AA54443	Secoisolaricresin
95	261	19.9	340	21	AA810741	H. ghiliani/B. me
96	260.5	19.9	273	21	AA54441	Secoisolaricresin
97	260	19.9	243	23	AB854107	Lactococcus lactis
98	259	19.8	253	22	AA036249	Pseudomonas aerugi
99	258	19.7	283	21	AA031552	Arabidopsis thalia
100	258	19.7	283	23	AB892823	Herbicidally activ

ALIGNMENTS

RESULT 1
AAW71471
ID AAW71471 standard: Protein: 261 AA.

AAW71471;
16-DEC-1998 (first entry)

ERAB protein.

Endoplasmic reticulum associated amyloid-beta peptide binding protein;
ERAB protein; amyloid-beta peptide; inhibitor; demyelinating disease;
neurodegenerative disorder; therapy; Alzheimer's disease; schizophrenia;
Down's syndrome; Parkinson's disease; Huntington's disease;
multiple sclerosis.

Homo sapiens.

MO9840484-A1.

17-SEP-1998.

12-MAR-1998; 98WO-US04935.

12-MAR-1997; 97US-0815225.

(UNCO) UNIV COLUMBIA NEW YORK.

Stern DM, Yan SD;

MP1, 1998-531524/45.

N-PSDB; AAV60576.

Endoplasmic reticulum associated amyloid-beta peptide binding
protein - inhibitors of which can be used to treat neurodegenerative
disorders

Claim 2; Fig 1D; 53pp; English.

This sequence is the endoplasmic reticulum associated amyloid-beta
peptide binding (ERAB) protein of the invention. The protein can be used
in a method for evaluating the ability of an agent to inhibit binding of
ERAB polypeptide to amyloid-beta peptide comprising: (a) incubating the
ERAB polypeptide, the agent and amyloid-beta peptide under binding
conditions; (b) determining the amount of amyloid-beta peptide bound to
ERAB polypeptide; (c) comparison of the amount of binding with results
from a control using no agent, so determining inhibition ability of the
agent. The inhibitors identified by the method can be used to treat a
neurodegenerative condition by administration of an agent that inhibits
binding of an ERAB polypeptide to amyloid-beta peptide, particularly
where the disease is Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, Huntington's disease, schizophrenia, a demyelinating disease, or
CC multiple sclerosis. The inhibitors can also be used to treat other
CC neurodegenerative conditions including those associated with ageing,
CC dentatorubral and pallidolysian atrophy, Machado-Joseph disease,
CC muscular dystrophy, senility, spinocerebellar ataxia type I, spinulbar
CC muscular atrophy, stroke, and trauma.
XX

Sequence 261 AA:

Query Match 100.0%; Score 1309; DB 19; Length 261;

Best Local Similarity 100.0%; Pred. No. 1.7e-119; Mismatches 0; Gaps 0;

Matches 261; Conservative 0; Indels 0; Gaps 0;

QY 1 MAACRSVGLVAVINVGASGLIATAEFLVVGASAVLDDIPNSGGEAKKLNQVF 60

Db 1 MAACRSVGLVAVINVGASGLIATAEFLVVGASAVLDDIPNSGGEAKKLNQVF 60

QY 61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYMLKKQHTLDFORVLDV 120

Db 61 APADVTSEKDVOTALALAKGFRVDVAVNCAGIAVASKTYMLKKQHTLDFORVLDV 120

QY 121 NLKGTFFVRLVAGEGQNEPDGQGRVITNTASVAAREGQVGAASASGIVGML 180

Db 121 NLKGTFFVRLVAGEGQNEPDGQGRVITNTASVAAREGQVGAASASGIVGML 180

QY 181 PIARDIAPIGIRMYTAPGLFGTPLLTSUPERVCNFLASQVFPRLGDPAEVAHLVQAI 240

Db 181 PIARDIAPIGIRMYTAPGLFGTPLLTSUPERVCNFLASQVFPRLGDPAEVAHLVQAI 240

QY 241 IENPFLNGEYIRLDGAIKMP 261

Db 241 IENPFLNGEYIRLDGAIKMP 261

RESULT 2
AAW67934
ID AAW67934 standard: Protein: 227 AA.

AAW67934;

25-MAR-1999 (first entry)

Fragment of human secreted protein encoded by gene 8.

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal;

immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;

inflammation; ischaemic shock; Alzheimer's disease; stenosis; AIDS;

cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Homo sapiens.

WO9842738-A1.

01-OCT-1998.

19-MAR-1998; 98WO-US05311.

30-MAY-1997; 97US-0050937.

21-MAR-1997; 97US-0041276.

21-MAR-1997; 97US-0041277.

21-MAR-1997; 97US-0041281.

21-MAR-1997; 97US-0042344.

30-MAY-1997; 97US-0048096.

30-MAY-1997; 97US-0048095.

30-MAY-1997; 97US-0048096.

30-MAY-1997; 97US-0048099.

30-MAY-1997; 97US-0048131.

30-MAY-1997; 97US-0048135.

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us-09-931-186-8.rag

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:19:21 ; Search time 39.6667 Seconds

(without alignments)
876.767 Million cell updates/sec

Title: US-09-931-186-8
Perfect score: 1309
Sequence: 1 MAACRSVKGLVAITIGAS.....ENPFLNGEYIRLDGAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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23: /SIDB2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1309	100.0	261	19	AAW71471
2	1146	87.5	227	20	AAW67934
3	1144	87.4	260	21	AAV32239
4	908	69.4	255	22	ABBS2988
5	664.5	50.8	388	18	AAW06513
6	361.5	27.6	244	23	ABP28011
7	351	26.8	243	23	ABP27345
8	326.5	24.9	243	19	AAW06070
9	326.5	24.9	243	21	AAI15706
10	326.5	24.9	243	22	AAU3767

11	326.5	24.9	243	22	AAU37988	Streptococcus pneu
12	325.5	24.9	243	22	AAW01032	CEE 35 protein seq
13	324.5	24.8	243	23	ABBS4087	Lactococcus lactis
14	318.5	24.3	245	22	AAU35328	Enterococcus faeca
15	317	24.2	257	22	AAU28344	Novel human secret
16	314	24.0	237	22	AAW50255	Human dehydratogen
17	313.5	23.9	241	22	AAW66397	Human dehydratogen
18	312	23.8	237	22	AAU28156	Putative P. abysssi
19	312	23.8	237	22	AAU28156	Novel human secret
20	310.5	23.7	248	21	AAI19928	Human oxidoreducta
21	303.5	23.2	247	23	AAV54422	Amino acid sequenc
22	301	23.0	247	21	ABBA4892	Listeria monocyrog
23	300.5	23.0	288	22	AAU28296	Bacillus megaterium
24	295	22.5	263	23	ABP39667	Novel human secret
25	294	22.5	262	22	ABG83032	Staphylococcus epi
26	293.5	22.4	267	22	AAW47459	S. epidermidis ope
27	292.5	22.3	262	22	AAW86537	Levodione reductas
28	291	22.2	315	17	AAW89323	G. suboxydans DSM
29	291	22.2	315	17	AAW89322	Rape leaf beta-ket
30	290.5	22.2	270	20	AAV41761	Rape seed beta-ket
31	290.5	22.2	270	21	AAW44317	Human PRO474 prote
32	290.5	22.2	270	21	AAW44317	Human PRO474 (UNOS
33	290.5	22.2	270	22	AAW28108	Human PRO474 prote
34	290.5	22.2	279	22	AAU18296	Novel human secret
35	289.5	22.1	244	21	AAV54421	Human endocrine po
36	289.5	22.1	244	22	AAU34533	Amino acid sequenc
37	288.5	22.0	246	12	AAU10974	E. coli cellular p
38	288.5	22.0	262	21	AAV44578	Acetoacetyl CoA re
39	288	22.0	263	22	AAU38499	Xylytol dehydrogen
40	287.5	22.0	263	22	AAU38499	Salmonella typhi c
41	287.5	22.0	246	10	AAW94157	Acetyl-CoA reducta
42	287.5	22.0	246	14	AAW32192	Sequence encoded b
43	287.5	22.0	246	20	AAV43310	Acetoacetyl-CoA re
44	287.5	22.0	246	21	AAV54423	Novel human secret
45	287.5	22.0	246	22	AAW71981	Human endocrine po
46	287.5	22.0	303	23	ABBS2824	Acetyl-CoA reducta
47	286.5	22.0	329	16	AAW71324	Herbicideidally activ
48	286.5	21.9	270	21	AAW42558	Acetyl-CoA reducta
49	283.5	21.7	270	21	AAV54415	Human ORF2322
50	282.5	21.6	253	23	ABBS4214	Secoisolaricresin
51	282	21.5	273	10	AAW94155	Lactococcus lactis
52	280.5	21.4	280	23	ABBS9249	Acetyl-CoA reducta
53	280.5	21.4	254	22	AAW49773	Herbicideidally activ
54	279.5	21.4	306	22	AAW81544	Protein with acetyl
55	278.5	21.3	241	12	AAW10679	S. epidermidis ope
56	278.5	21.3	242	12	AAU05920	Acetoacetyl CoA re
57	277	21.2	244	23	ABP39686	Propionibacterium
58	276	21.1	274	22	AAW81318	Staphylococcus epi
59	276	21.1	258	22	AAW92682	Human AFP protein
60	276	21.1	258	22	AAW92682	C glutamincum prote
61	275	21.0	285	22	AAW34648	Corynebacterium gl
62	274.5	21.0	286	14	AAW74761	E. coli cellular p
63	274.5	21.0	286	14	AAW74761	Acetoacetyl CoA re
64	274	20.9	254	22	AAW47522	(R)-2-octanolol dehy
65	273.5	20.9	269	23	ABBS9248	Herbicideidally activ
66	273.5	20.9	206	23	AAU09345	Short-chain dehydr
67	272.5	20.8	249	23	ABP39980	Staphylococcus epi
68	272.5	20.8	249	23	AAU77210	Staphylococcus epi
69	271.5	20.7	282	22	AAU37095	Consensus protein
70	269.5	20.6	286	22	AAU36267	Staphylococcus aur
71	269.5	20.6	286	22	AAU36267	Pseudomonas aerugi
72	269.5	20.6	251	22	AAU34193	Staphylococcus aur
73	269.5	20.6	251	22	AAU34193	Staphylococcus aur
74	269.5	20.6	246	21	AAH15707	Staphylococcus aur
75	268.5	20.5	246	22	AAU33965	Staphylococcus aur
76	268.5	20.5	246	22	AAU33965	Staphylococcus aur
77	268	20.5	246	22	AAU33965	Staphylococcus aur
78	267.5	20.4	336	16	AAW06488	Staphylococcus aur
79	266.5	20.4	242	22	AAU35381	Staphylococcus aur
80	266.5	20.4	242	22	AAU35381	Staphylococcus aur
81	266.5	20.4	266	21	AAV92809	Maize T52 sequence
82	266.5	20.4	267	21	AAV92809	Haemophilus influe
83	266	20.3	308	21	AAW35504	Human OXRE-6 Hom
			254	23	AAW35504	Arabidopsis thalia
			254	23	AAW35504	Arabidopsis thalia
			254	23	AAW35504	Listeria monocyrog

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Search completed: June 23, 2003, 14:35:42
Job time : 13.1667 secs

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REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 270:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e
US-08-858-207A-270

Query Match 20.5%; Score 268; DB 4; Length 186;
Best Local Similarity 38.7%; Pred. No. 5.8e-22;
Matches 74; Conservative 23; Mismatches 72; Indels 22; Gaps 5;

QY 15 ITGGASGIGLATAERLYGOGASAVLLDLPNSGGE-----AQAKKIGNCVFAPADVTSE 68
DB 10 ITGSSRGIGLAIAMKFAQAGANIVL-----NSRGAISELLAEFSNIGIKVPIISGDVSDF 65
QY 69 KDVOFTALALAKGKGRDVAVNCAGIYASKTYNLKKGQTHLEDFORVLDVNLMTFNV 128
DB 66 ADARMTDQALAEISYDVNLNNGI--TODTILMK---TEADFEKVLKVLGTAFNM 119
QY 129 IRLVAGEMGONPDGOGGVYINTASVAEFGVGQAAYSASKGIVGMLPIARDLAP 188
DB 120 TQSVL-----KPMKRAKREGALIMSSVGMIGQANTAAKAGLIGTTKVARAYAS 173
QY 189 IGIRVMTIAPG 189
DB 174 RIRVMTIAPG 184

RESULT 24

US-08-440-856A-3
Sequence 3, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOENSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-3

Query Match 20.4%; Score 267.5; DB 1; Length 337;
Best Local Similarity 30.9%; Pred. No. 1.7e-21;
Matches 88; Conservative 44; Mismatches 112; Indels 41; Gaps 6;

QY 6 RSVKGLVAVITGGASGIGLATAERLYGOGASAVLLDLPNSGGEAQAKKIGNCVFAPADY 65
DB 51 KRDKGVAVITGGARGIGAIYELPAKHGARVADIDDAAGALASAGPOVPSVFRCDY 110
QY 66 TSEKDVOTLALAKGE-GRVDVAVNCAGIYASKTYNLKKGQTHLEDFORVLDVNLMTG 124
DB 111 SVEDDVRAVDNALSHSGRLDYCNNGV-LGRQTRARSLTSPDAEFRLVFNALG 169
QY 125 TENVILVAGEMGONPDGOGGVYINTASVAEFGVGQAAYSASKGIVGMLPIAR 184
DB 170 PALGMKHAARAPR-----RAGSLVSAVAAYLGLGPHAYTASKHAIVGLTKNAAC 223
QY 185 DIAPIGIRVMTIAPGLFTPL-----TSLP-----EK 212
DB 224 ELRAHGVRYNCSPFVATPMLINARQGHDATAADRDLDLDVYVPSQVEKME 283
QY 213 VCNFLASQVPPSRIGDPAEYALVQATLENPFLNGEYIRLDGAI 257
DB 284 VVGLATLKGPTLRPRDIAE-AVLFLASDEARYISGHNLVVDGCV 327

RESULT 25

US-09-504-358-14
Sequence 14, Application US/09504358
Patent No. 6365376
GENERAL INFORMATION:
APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIA
FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/504,358
CURRENT FILING DATE: 2000-02-15
EARLIER APPLICATION NUMBER: 60/120,702
EARLIER FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 256
TYPE: PRT
ORGANISM: Brevibacterium sp HCU
US-09-504-358-14

Query Match 20.3%; Score 266; DB 4; Length 256;
Best Local Similarity 30.9%; Pred. No. 1.6e-21;
Matches 82; Conservative 39; Mismatches 116; Indels 28; Gaps 8;

QY 10 GLVAVITGGASGIGLATAERLYGOGASAVLLDLPNSGGEAQAKL---GNNCVFAPADY 66
DB 6 GKVAVITGGAGMGRIOSELVASEGAQVAVVDNEQEGATADATRASGVANYWKLDVS 65
QY 67 SENDVOTLALAKGKGRDVAVNCAGIYASKTYNLKKGQTHLE--DFQVLDVNLMTG 124
DB 66 DESEVEIVSDIAKRGAINVLNNAQVGAOK-----PHEIDERLDLVLSDVKG 118
QY 125 TENVILVAGEMGONPDGOGGVYINTASVAEFGVGQAAYSASKGIVGMLPIAR 184
DB 119 VEFMTGHCIPFKQ---AG--GATVNFASLYGLVSGEELPYHAKAAVVALTKQAV 172
QY 185 DIAPIGIRVMTIAPGLFTPLTSLPEK-----VCNFLASQVPPSPRLDPAEY--AH 235
DB 173 TYGPNIRVNAVAPGILPLVKEGSRGPDGLDGYTKLMGAKHPL-GRVGTPEEVAAT 231
QY 236 LVQATLENPFLNGEYIRLDGAI 260
DB 232 LFLASEASFTIGAVLPVDGQYTAQ 256

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FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 67,695
FILING DATE: 29-JUN-1987
SEQ ID NO: 4
LENGTH: 273
5512669-4

Query Match 21.6%; Score 282.5; DB 6; Length 273;
Best Local Similarity 31.5%; Pred. No. 2.5e-23;
Matches 90; Conservative 42; Mismatches 91; Indels 63; Gaps 11;

12 VAVITGASGGLATTAERLVGQASAVLLDLPNSGGEAQAANKLGNCFAPPA-----63
4 VALVTGSGRGIG-----AAISIALKAGAYKASYSAGNDAAKPFKAETGIAY 51
64 ---DVTSEKDVOTLALAKKGFGRVDVAVNCAGIATAVASKTYNLKKGOTH--TLEDPORYL 118
52 YKMDVSTECACVEGIAKAEADLGFDLVNNAIGIT-----KDAHFHKKTPDQWNAVI 103
119 DVNLGTFENVL-----RLV-----AGEMGQ-NEPDQGOR---GVYIN 152
104 NTNLGLFNMTHPVWSGMRDSFGRIYVSSINGQKGMQANYSVSMGRDSEFGRIYN 163
153 TASVAAREGQVGOAAYSKSGIGVMTLPARDLAPIGIRVMTIAPGLFGLTSLPEK 212
164 ISSINGQGMQGMQANYSAKAGDVGFTKALAGSAGAGITVNAICPGYIGTEWYRAIPEK 223
213 VCN-FLASQVFPFRLDPAEYAHV--QATIEPFLNGEVIRIDG 255
224 VLNERIIPQIV-GRLGEPDEIARIYVFLASDEAGFITGSIISANG 268

RESULT 18
US-09-134-001C-4431
Sequence 4431, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4431
LENGTH: 274
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4431

Query Match 21.3%; Score 278.5; DB 4; Length 274;
Best Local Similarity 31.7%; Pred. No. 7.1e-23;
Matches 85; Conservative 45; Mismatches 93; Indels 45; Gaps 8;

12 VAVITGASGGLATTAERLVGQASAVLLDLP-----NSGGEAQAANKLGNCF 60
10 IAVITGASTGIGASAVALLAEGAHVLAIDISDLEETVQSINDNGKATYRY-----63
61 APADVTSEKDVOTLALAKKGFGRVDVAVNCAGIATAVASKTYNLKKGOTH--TLEDPORYL 118
64 ---DISDQVYKQSEKIAOEFGRVDFVFNNAVDNGA-----GRHEPVEVFPKIM 113
119 DVNLGTFENVIRLVAGEMQNEPDQGORVYINTASVAAREGQVGOAAYSKSGIGYGM 178
114 AVDMGTLVYKFL-----PLMKOGGSIINTASSGGAADLIRSGYIAAGGYINF 166
179 TLPIARDLAPIGIRVMTIAPGLFGLTSLPEKVCNPLASQ--VEPFRGLDPA 231
167 TKSIAIEYGRNIRANAIAPGITEPIVDNLGAGTSDEBAGOTFRENCKWTVPLGRLGPD 226

QY 232 EYAHVQ--ATIEPFLNGEVIRIDGAI 257
DB 227 EVGKLVAFLASDSSFTGETIRIDGCV 254

RESULT 19

US-09-134-001C-4825
Sequence 4825, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4825
LENGTH: 249
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4825

Query Match 20.9%; Score 273.5; DB 4; Length 249;
Best Local Similarity 29.1%; Pred. No. 2.2e-22;
Matches 74; Conservative 54; Mismatches 105; Indels 21; Gaps 6;

QY 13 AVITGASGGLATTAERLVGQASAVLLDLPNSGGEAQA-----KRLGNVCVAPADVTS 67
DB 10 ALVTGASRGIGRSIALQLAEEGYN-VAVYAGSKDKAEAVVERIKAGVESPAIQANVAK 68
68 EKDVOTLALAKKGFGRVDVAVNCAGIATAVASKTYNLKKGOTHLEDFQRYLVNLMGTEN 127
69 GDEVKEMIKRVVSQFSGVDVAVNNAIGITKDNLMRKE-----QEMDVITDNLKGVFN 122
128 VIRLVAGEMQNEPDQGORVYINTASVAAREGQVGOAAYSKSGIGVMTLPARDIA 187
123 CIOKVPQOMLRQ-----RSGAIINTLSIYAGANGNGQANYATKAGVIGLRTAREDA 176
QY 188 PIGIRVMTIAPGLFGLTSLPEKCNFLASQVPEPSRLGDPAEYAHVQAIIEE--PE 245
DB 177 SRGITVNAVAPGFTVSDMTNALSDDLKQMLEQIPL-KRFGEDTIDANTVAFASPKAY 235
QY 246 LNGEVIRIDGAIEM 259
DB 236 ITGOTIHVNGMYM 249

RESULT 20

US-09-238-481-2
Sequence 2, Application US/09238481
Patent No. 6110704
GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Daniel
TITLE OF INVENTION: FabG
FILE REFERENCE: GM10192
CURRENT APPLICATION NUMBER: US/09/238,481
CURRENT FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-238-481-2

Query Match 20.6%; Score 269.5; DB 3; Length 246;

APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6280997ember-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6280997man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5372.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-729-594A-13

Query Match 21.8%; Score 285.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 9.8e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;
QY 9 KGLVAVITGGASGLTAEIARLVGOGASAVLLDLPNSGGEAOKKIGNNCVFAPADVTSE 68
DB 4 EKKIALVTGASRGIGRAIETIARLGKVIQTATSENGAQAISDYIGANGKGLMLNTVP 63
QY 69 KDVOITALAKKRGKRDVAVNCAGIYASKTYNLKKGGTHLTEDFORVLDVNLMGTFNY 128
DB 64 ASIESVLEKIRAEFGVDILVNNAGITRDNLMLMKD-----EWMNIIETINLSVTRL 117
QY 129 IRLVAGEMQNEPDGQGVIIINTASVAAFEQVGOAAYSASKSGIVGMLPIARDLAP 188
DB 118 SKAVRAMMK-----RHGRITIGSVGTMGNGGQANAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLFETPLTSLPEKVCNPLASQVPPSRIGDPAEYAHLYQ--AIENPFL 246
DB 172 RGIIVNVVAPGFETIDTRALSDQDAGILAOVP-AGRLGGAQEIANAVALASDEAYI 230
QY 247 NGEVIRLDGAIIM 259
DB 231 TGETLHVNGMYM 243
RESULT 16
US-08-937-993-13
Sequence 13, Application US/08937993
Patent No. 6399344
GENERAL INFORMATION:
APPLICANT: Eriksson, Olaf Simon, Andras; Romert, Anna
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993

FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6399344ember-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
US-08-937-993-13

Query Match 21.8%; Score 285.5; DB 4; Length 244;
Best Local Similarity 29.6%; Pred. No. 9.8e-24;
Matches 75; Conservative 50; Mismatches 113; Indels 15; Gaps 4;
QY 9 KGLVAVITGGASGLTAEIARLVGOGASAVLLDLPNSGGEAOKKIGNNCVFAPADVTSE 68
DB 4 EKKIALVTGASRGIGRAIETIARLGKVIQTATSENGAQAISDYIGANGKGLMLNTVP 63
QY 69 KDVOITALAKKRGKRDVAVNCAGIYASKTYNLKKGGTHLTEDFORVLDVNLMGTFNY 128
DB 64 ASIESVLEKIRAEFGVDILVNNAGITRDNLMLMKD-----EWMNIIETINLSVTRL 117
QY 129 IRLVAGEMQNEPDGQGVIIINTASVAAFEQVGOAAYSASKSGIVGMLPIARDLAP 188
DB 118 SKAVRAMMK-----RHGRITIGSVGTMGNGGQANAAKAGLIGFSKSLAREVAS 171
QY 189 IGRVMTIAPGLFETPLTSLPEKVCNPLASQVPPSRIGDPAEYAHLYQ--AIENPFL 246
DB 172 RGIIVNVVAPGFETIDTRALSDQDAGILAOVP-AGRLGGAQEIANAVALASDEAYI 230
QY 247 NGEVIRLDGAIIM 259
DB 231 TGETLHVNGMYM 243
RESULT 17
5512669-4
Patent No. 5512669
APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
TITLE OF INVENTION: GENE ENCODING BACTERIAL ACETOACETYL-COA
REDUCTASE
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,667
FILING DATE: 29-Aug-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 124,570
FILING DATE: 20-SEP-1993
APPLICATION NUMBER: 944,488
FILING DATE: 03-NOV-1992
APPLICATION NUMBER: 566,535

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RESULT 11
US-08-793-035-10
; Sequence 10. Application US/08793035
; Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Sladas, Antoni R.
APPLICANT: White, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Elborough, Kelvin
APPLICANT: Pentem, Phillip A.
TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 941622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB95/01678
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT-132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713.787.1400
TELEFAX: 713.787.1440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-793-035-10

Query Match 22.2%; Score 291; DB 3; Length 315;
Best Local Similarity 30.5%; Pred. No. 3,6e-24;
Matches 80; Conservative 44; Mismatches 116; Indels 22; Gaps 6

4 ACRSVKGLVAVITGASGLGLTARLRYGQASAVLLDLPNSGGAA-----QAKLGNNC 58
Db 66 AVPKVESPVVVVTGASRIGKAIALSL-GRAGCKVLVNRASAKAEVYSKQIEAVYGGQA 124

59 VFAPADVYSEKDVQALALAKGKFGRVDAVAVACAGIAVASKTYNKKGTHTLEDFORVL 118
Qy 125 ITFGSDVSKEDAEVEMKMTAIDAWGTIDVYVYVNNAGITDILLIRKKSG-----WDEVI 178
Db 119 DYNLMGTNNVIRLVAGEGQNEPDGQGRGVYIINASVAAFPGVGYQQAYSKSGGIYGM 178
Qy 179 DLNLTGVFLCQQAATIKMKR-----RKGRITINIASVGLIGNGQAVYAAKAGVIGF 232
Db 179 TLPIARDLAPIGIRVYTAIPGDFGLTSLPEKYCNFLASQVPPPSRLGDAPEAYAHVQ 238
Qy 233 SKTAREASRNINNVVCPGFIASDMFAKLGEDMEKKTLIGIPL-GRYGGQEDVAGVIE 291
Db 239 AIIENP---FLNGEYIRLDGAI 257
Qy

```

```

Db          292 FLALSPASAYITGQAFITDGI 313

RESULT 12
5229279-7
; Patent No. 5229279
; APPLICANT: PEOPLES, OLIVER P.; SINSKEY, ANTHONY J.
; TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL POLYESTER
; BIOPOLYMERS
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/556,535
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 67,695
; FILING DATE: 29-AUG-1987
; SEQ ID NO: 7
; LENGTH: 246
5229279-7

Query Match      22.0%; Score 287.5; DB 6; Length 246;
Best Local Similarity 31.9%; Freq. No. 6e-24;
Matches 81; Conservative 45; Mismatches 109; Indels 19; Gaps 7;

QY      12 VAVITGASGLGATLERTLVGGGASVLLDLPNSGSE---AQARKIGNNCVFAPADYTS 67
Db      5 IAVYTGGMGSIQALICORLAKKDFRVYAGGCPSPRREKULBQCKALGFDFIASGNAVAD 64
QY      68 EKDVQTLALAKKRFQGVVDYAVNACAGAAVASKTYN.LKKGFHTLEDPQGVLDVNLGMFEN 127
Db      65 WDSKTITAFDKYKSBVEGVLDVLIINNAGI---TRDYVERK---MTRADMAYIDITNLTSLFN 118
QY      128 VIRLVAGEMGONEPDGGGQGVIIINTASVAEFGQVGOAAYSASKGIVGKTLPIARDIA 187
Db      119 VTKGVIDGMA---DRGW--GRIVNISVYNGCKGFGCQNTYSIAKAGLIGFTMALAOEYVA 172
QY      188 PIGIRWETIAPGLEFPGFLTSLPEKYNFLFASQVPPSPRLGDPAEYAHVQAIT--ENPF 245
Db      173 TKGTVTATVSPGIATIMYKAIKQDVLDKIVATIPV-KRLGLPQLFASICANLSESESGF 231
QY      246 LMGVIRLDGAIRM 259
Db      232 STGADFSLNGLHM 245

RESULT 13
US-08-375-962B-13
; Sequence 13, Application US/08375962B
; Patent No. 5731195
; GENERAL INFORMATION:
; APPLICANT: SIMON, ANDRAS; HELLMAN, ULE; WERNSTEDT,
; APPLICANT: CHRISTER; ERIKSSON, ULF.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecule
; TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
; TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63
; TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM type: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect (ASCII standard)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,962B
; FILING DATE: 20-January-1995
; CLASSIFICATION: 435

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Page 5

QY 6 RSVGLIVAVITIGGASGLATAEERLVGGASVLLDPLPSG---GGAOKKLTGNNOVFAP 62

Db 3 KKFNGKVCVLTGAGAGNIGCATPRLAEESTALALDMDNREALEKAAVSAREKVEARSYV 62

QY 63 ADVTSSEKVTOTALAKGFRFVYDVAVNCAGIYAVASKYTNLKGGTHTLEDFQRYADVNL 122

Db 63 CDVTSSEAVIGTVDSVDFDKIDFLFNNAVYOGA-----FAYQDYPSDDFARYLTINV 117

QY 123 MGTNVTIVLVAGEM-GONEPDGGQGVLIINTASVAFEQGVQGAAYASAKGIVMTLP 181

Db 118 TGAFFVLAVASQOMTTON-----YGRIVNTASMAAGVGGPRMAAYGASKGIITALTER 170

QY 182 IARDLAPITGIRVMTAPGLF-----GTPLNLSLPEKVCNLFASQPPFS 225

Db 171 AALDLDPIRINRNAISPGYMGFEMMEROVELOAKYGSQIFSTDPKRVAAQOMTGVPDM-R 229

QY 226 RLGDPAEYAHLYQAI--ENPLFNGEVIRLDG 255

Db 230 RYGDINEITPGVAVAFLLGDDSSFTMTGVNLTPIAG 261

[illegible]

Thu Jun 26 06:55:11 2003

us-09-931-186-8.ra1

Page 4

ADDRESS: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-4

Query Match 22.9%; Score 299.5; DB 1; Length 333;
Best Local Similarity 32.5%; Pred. No. 4.4e-25;
Matches 92; Conservative 46; Mismatches 106; Indels 39; Gaps 5;

QY 6 RSVGLVAVITGGASGLATAEALVVGOGASAVLLDIPNSGGEQAOKLGNVCYFAPADY 65
DB 50 KRLSKVAIVTGGARGGEALVRLVHGAKVVIADIDDAAGELAAALPHEGVFVCDV 109
QY 66 TSEKDVOTALAKRGKRVDAVAVNACAGIAVASKTYNLKQQTHTLDFQVLDVNLG 125
DB 110 SVEEDVERAVRAVARGRLDVLNNGV-LGROTBAKSTLSFDAGEPRVLEKVNALGA 168
QY 126 FNVIRLVAGKQNEPDGGRVYINTASVAEEGCGAASASGIGYKTLPIARD 185
DB 169 ALGKHAALAMTOR-----RAGSIISVAVAGVGLGPRHAYASKHAIVGLKNACE 222
QY 186 LAPGIRMTAPGLFGPLP-----TSLP-----BKVC 214
DB 223 LGAGIRVNCISPGVATPMLINAMRGHDASTADADADIDDIATVPSQEVKMEV 282
QY 215 NFLASQVFPRLDPAEVAHLYOAITENPFLNGEVIRLDGAI 257
DB 283 RGLATLKGAITLRPRDIAE-AALFLASDSDSYISGHNLVYDGV 324

RESULT 7
US-08-815-225-4
Sequence 4, Application US/08815225
Patent No. 6268479
GENERAL INFORMATION:
APPLICANT: Stern, David M.
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
TITLE OF INVENTION: BINDING (EPAB) POLYPEPTIDE AND METHODS FOR INHIBITING
TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/55209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-815-225-4

Query Match 22.8%; Score 299; DB 4; Length 255;
Best Local Similarity 33.6%; Pred. No. 3.3e-25;
Matches 85; Conservative 47; Mismatches 101; Indels 20; Gaps 8;

QY 8 VKGLVAVITGGASGLATAEALVVGOGASAVLLDIPNSGGEQAOKLGNVCYFAPADY 67
DB 4 LSKRTVITGGANGLAEAARQVAVAGARVLDVDEGAAFTARLGDARVQHLDT 63
QY 68 EKVQOTALAKRGKRVDAVAVNACAGIAVASKTYNLKQQTHTLDFQVLDVNLG 127
DB 64 EEDMORVAVAREFESVGLVNNAGISTGMFL-----ETSEVERKRVVDINLTGFT 117
QY 128 VIRLVAGKQNEPDGGRVYINTASVAEEGCGAASASGIGYKTLPIARD 187
DB 118 GAKTVIPAM---KXAGG--GSIVNISAAGLMGLALTSYGASKVGLSKLAVELG 171
QY 188 PIGIRMTAPGLFGPLP--TSLPEKVCNPLASQVFPFSRLG-DPAEVAHLYOAIT 242
DB 172 TDRIRVNSVHPGMYTPMTAETGIRGEGSY--PNTPM-GRVGENEGETAGAVKILSDT 228
QY 243 NPFLNGEVIRLDG 255
DB 229 SSVYTGAEALVDG 241

RESULT 8
US-09-134-001C-4512
Sequence 4512, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4512
LENGTH: 263
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4512

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
;; FILE REFERENCE: 25885-1651
;; CURRENT APPLICATION NUMBER: US/09/347,878C
;; CURRENT FILING DATE: 1999-07-06
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 50
;; LENGTH: 261
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-347-878-50

Query Match 100.0%; Score 1309; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 7e-138;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACRSVKGLVAVITGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCVF 60
DB 1 MAACRSVKGLVAVITGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCVF 60
QY 61 APADVTSEKDVOTLALAKGFGYDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDV 120
DB 61 APADVTSEKDVOTLALAKGFGYDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDV 120
QY 121 NMGTEVIRLVAGEMQNEPDGGQGVIIINTASVAAFEGQVGAAYASAKSGIVGML 180
DB 121 NMGTEVIRLVAGEMQNEPDGGQGVIIINTASVAAFEGQVGAAYASAKSGIVGML 180
QY 181 PIARDLAPIGIRWTTAPGFGLTSLPEKYCNFLASQVPPSRDGAETAYHVOAI 240
DB 181 PIARDLAPIGIRWTTAPGFGLTSLPEKYCNFLASQVPPSRDGAETAYHVOAI 240
QY 241 IENPFLNGEVIIRLDGAIRMOP 261
DB 241 IENPFLNGEVIIRLDGAIRMOP 261

RESULT 4
US-08-980-832-41
;; Sequence 41, Application US/08980832B
;; Patent No. 6291204
;; GENERAL INFORMATION:
;; APPLICANT: Pasamontes, Luis
;; APPLICANT: Tsygankov, Yuri
;; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
;; FILE REFERENCE: Improved Fermentative Carotenoid
;; CURRENT APPLICATION NUMBER: US/08/980,832B
;; CURRENT FILING DATE: 1997-12-01
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 41
;; LENGTH: 388
;; TYPE: PR1
;; ORGANISM: Flavobacterium sp. R1534
US-08-980-832-41

Query Match 50.8%; Score 664.5; DB 4; Length 388;
Best Local Similarity 55.5%; Pred. No. 1.1e-65;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGASGLGATAERLVGGASAVLLDLPNSGGEAOKKLGNNCVFAPADVTSE 67
DB 143 IEGRVFVVTGAASGLGASASAMLAQGGAKVVLADL-----AEKDAPEGAVHAAADVTD 196
QY 68 EKDVOITALALAKGFGYDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDVNLMGTFN 127
DB 197 ATAAGTALALATDFGRDLGVNCGAIAPEARM--LRDGHGHDSTARRAVTILNISFN 254
QY 128 VIRLVAGEMQNEPDGGQGVIIINTASVAAFEGQVGAAYASAKSGIVGMLPIARDLA 187
DB 255 MARLAARMAHNEPVR--GERGVIVNTASIAADQOIQVAVYAAASKAGVAGWTLPMAADLA 313
188 PICTRYMTIARGTGTETITSI PRKYCNFLASQVPPSRDGAETAYHVOAITFNFPTN 247

DB 314 RHGIRVMTIARGTGTETITSI PRKYCNFLASQVPPSRDGAETAYHVOAITFNFPTN 247
QY 248 GEVIRLDGAIRMOP 261
DB 374 GEVIRLDGAIRMOP 387

RESULT 5
US-09-239-052-2
;; Sequence 2, Application US/09239052
;; Patent No. 6346395
;; GENERAL INFORMATION:
;; APPLICANT: Holmes, David J.
;; APPLICANT: Zhong, Yiyi
;; APPLICANT: Debouck, Christine
;; APPLICANT: Jaworski, Deborah D.
;; APPLICANT: Wang, Min
;; APPLICANT: Warren, Richard L.
;; APPLICANT: Kosmatka, Anna L.
;; APPLICANT: McDevitt, Damien
;; APPLICANT: Ingraham, Karen A.
;; APPLICANT: Chalke, Alison F.
;; APPLICANT: So, Chi Young
;; APPLICANT: Wallis, Nicola G.
;; APPLICANT: Pearson, Stewart C.
;; TITLE OF INVENTION: FdG
;; FILE REFERENCE: GM10191
;; CURRENT APPLICATION NUMBER: US/09/239,052
;; CURRENT FILING DATE: 1999-01-27
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 2
;; LENGTH: 243
;; TYPE: PR1
;; ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 24.9%; Score 326.5; DB 4; Length 243;
Best Local Similarity 35.1%; Pred. No. 2.6e-28;
Matches 88; Conservative 56; Mismatches 104; Indels 23; Gaps 6;

QY 15 ITGASGLGATAERLVGGASAVLLDLPNSGGE-----AOAKKLGNNCVFAPADVTSE 68
DB 10 ITGSSGIGIDLALAKHKAQAGANIVL-----NSRGAISEELAFSNVGIKVVIFISDVDF 65
QY 69 KDVOTLALAKGFGYDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDVNLMGTFN 128
DB 66 ADARKMIDQALIELGSDVDLVNNAgi--TQDTLMLK-----TEADEKVLKYNLGAERFM 119
QY 129 IRLVAGEMQNEPDGGQGVIIINTASVAAFEGQVGAAYASAKSGIVGMLPIARDLA 188
DB 120 TQSVL-----KRMKARAGATINMSVGLMGNTQGANVYASAKGLIGFTSVAREVAS 173
QY 189 IGRVMTIARGTGTETITSI PRKYCNFLASQVPPSRDGAETAYHVOAITFNFPTN 247
DB 174 RNRVAVIAPGMIESDMTALISDKIKREATLQIPM--KEFGQAEQVADLVFLAGODYLTG 232
QY 249 EVIRLDGAIRMOP 259
DB 233 QVTAIDGGLSM 243

RESULT 6
US-08-440-856A-4
;; Sequence 4, Application US/08440856A
;; Patent No. 5750873
;; GENERAL INFORMATION:
;; APPLICANT: DELAPORTA, STEPHEN L.
;; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
;; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESSES:

ALIGNMENTS

RESULT 1

US-08-815-225-2
; Sequence 2, Application US/08815225
; Patent No. 6268479
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,225
; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-815-225-2

Query Match 100.0%; Score 1309; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 7e-138;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MAACRSVKGIVAVITGGASGLGATAEKLVGOGASAVLLDIPNSGGEAQAQKLNQCV 60
1 MAACRSVKGIVAVITGGASGLGATAEKLVGOGASAVLLDIPNSGGEAQAQKLNQCV 60
61 APADVTSEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDV 120
61 APADVTSEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDV 120
61 APADVTSEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDV 120
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121 NMGTFTNIRLVAGEMGNEPDGOGRGVINTASVAAFEGOVGOAAYSASKGIVGML 180
181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEVAHLVQAI 240
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181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEVAHLVQAI 240
241 IENPFLNGEYIRLDGAIKMP 261
241 IENPFLNGEYIRLDGAIKMP 261

RESULT 2

US-08-815-225-3

US-08-815-225-3
; Sequence 3, Application US/08815225
; Patent No. 6268479
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
; TITLE OF INVENTION: NEURODEGENERATIVE CONDITIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,225
; FILING DATE: 12-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-815-225-3

Query Match 100.0%; Score 1309; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 7e-138;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MAACRSVKGIVAVITGGASGLGATAEKLVGOGASAVLLDIPNSGGEAQAQKLNQCV 60
1 MAACRSVKGIVAVITGGASGLGATAEKLVGOGASAVLLDIPNSGGEAQAQKLNQCV 60
61 APADVTSEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDV 120
61 APADVTSEKDVQALALAKGKFRVDVAVNCAGIAVASKTYNKKGTHTLEDFORVLDV 120
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181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEVAHLVQAI 240
181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEVAHLVQAI 240
181 PIARDLAPIGIRVMTIAPGLFTPLTSLPEKVCNFIASQVFPFSLGDPAEVAHLVQAI 240
241 IENPFLNGEYIRLDGAIKMP 261
241 IENPFLNGEYIRLDGAIKMP 261

RESULT 3

US-09-347-878-50
; Sequence 50, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong

Thu Jun 26 06:55:11 2003

us-09-931-186-8.rat

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:24:27 ; Search time 12.1667 seconds

(without alignments)
631.182 Million cell updates/sec

Title: US-09-931-186-8
Perfect score: 1309
Sequence: 1 MAACRSVKGLAVITGAS.....ENPLNGEIVRLDQAIKMP 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents, AA: *
1: /cgn2_6/ptodata/1/1aa/5A.CONB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.CONB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.CONB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.CONB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCRTUS.CONB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1309	100.0	261	4	US-09-347-878-50 Sequence 50, Appli
4	664.5	50.8	388	4	US-08-980-832-41 Sequence 41, Appli
5	326.5	24.9	243	4	US-09-233-052-2 Sequence 2, Appli
6	299.5	22.9	333	1	US-08-440-856A-4 Sequence 4, Appli
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8	295	22.5	263	4	US-09-134-001C-4512 Sequence 6, Appli
9	292.5	22.3	262	4	US-09-363-189B-6 Sequence 9, Appli
10	291	22.2	315	3	US-08-793-035-9 Sequence 9, Appli
11	291	22.2	315	3	US-08-793-035-10 Sequence 10, Appli
12	287.5	22.0	246	6	5229279-7 Patent No. 5229279
13	285.5	21.8	244	1	US-08-375-962B-13 Sequence 13, Appli
14	285.5	21.8	244	1	US-08-562-114B-13 Sequence 13, Appli
15	285.5	21.8	244	4	US-08-729-594A-13 Sequence 13, Appli
16	285.5	21.8	244	4	US-08-937-993-13 Sequence 13, Appli
17	282.5	21.6	273	6	5512659-4 Patent No. 5512659
18	278.5	21.3	274	4	US-09-134-001C-4431 Sequence 4431, Ap
19	273.5	20.9	249	4	US-09-134-001C-4825 Sequence 4825, Ap
20	269.5	20.6	246	3	US-09-238-481-2 Sequence 2, Appli
21	269.5	20.6	246	3	US-09-572-810A-2 Sequence 2, Appli
22	269	20.6	231	4	US-09-134-001C-4397 Sequence 4397, Ap
23	268	20.5	186	4	US-08-858-207A-270 Sequence 270, App
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25	266	20.3	256	4	US-09-504-358-14 Sequence 14, Appli
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PRIOR APPLICATION NUMBER: 60/085697

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QY 228 GDPAEY-AHLVOAIIENPLNG-EVIRLDGA 256
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219 GQPAEVGAAVFLASEANFTGIELVLTGGA 249

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Sequence 468; Application us/09978192A
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrata, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertslen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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QY 61 APADYTSKEDYOTALALAKRGGRVDAVNCAGIAVASKTYNLRKQOTHTLEDFQVLDV 120
DB 59 ILCDVTOEDDVKTIVSETIRRGRLDCVNNAGHHPD-----QREPTSAQGFROLLEL 113
QY 121 NLMGTFNNVIRLVAGEMGNEPDGGRGVYIINTASVAFEGOVGAASASAKGIVGTL 180
DB 114 NLGTYTTLTKIALPYLRKSQ-----GNVINTSLVGALIQARVPVATKGAVTATK 166
QY 181 PIARDLAPIGRVMTIAPGLFETPLTSLPERVCNFIASQVFP-----SRL 227
DB 167 ALALDESPPYGRVNVNIGSNITWPLME-----LALMDPPRATIREGLAQPLGRM 218
QY 228 GDPAEY-AHLVQATITENPLNG-EYIRLDGA 256
DB 219 GQPAEYGAAYFLASEANCTGIELLVYGA 249

RESULT 24
US-09-978-697-468
Sequence 468, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697

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us-09-931-186-8.rapb

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; TYPE: PRT
; ORGANISM: Bacillus megaterium
US-09-479-040-9

Query Match      23.0%; Score 301; DB 9; Length 247;
Best Local Similarity 29.1%; Pred. No. 1,3e-19;
Matches 78; Conservative 59; Mismatches 93; Indels 38; Gaps 9;

QY 7 SVKGLVAVITGASGLLTAERLYVGG-----ASAVLLDLPNSGGEQAKK 53
DB 3 TLQKRVAVITGSGSGLAATRELASGVAVAVNNSSKSAEYKEIDNNGEA-----58
QY 54 LGNNCFAPADVTSEKVOGTALALAKGFRVDVAVNCAIYASAKTYNLK-K-GQHTLE 112
DB 59 -----IAVQADVSVYDQAKHLIEETKAFGLDILVNNAGI---TRDRSFKLGE-----E 106
QY 113 DFOKVLVNMKGTNNVRLVAGENGQNEPDGQGGVITINTASVAEFGVQGAAYSASK 172
DB 107 DMKRVIDVNLHSYNTTSALTLESE---GGR---VINISITGAGSGFGQTNISAAK 160
QY 173 GGIYGMTLPARDLAPIGIRVMTIAPGLFGLTSLPEKYCNFLASQVFPFRLGDPAE 232
DB 161 AGMLGFRKSLALELAKGVTVNAICPGFIETEMVAIPEDVAKIVAKIP-TRLGLAAE 219
QY 233 YAH-LVQAIENPFLNGEVRIDGAIKM 259
DB 220 IARGVYLAKDGAYITGQNLINGLYM 247

RESULT 20
US-09-773-748-1
; Sequence 1, Application US/09773748
; Publication No. US20020187537A1
; GENERAL INFORMATION:
; APPLICANT: Masaru
; TITLE OF INVENTION: Levodione reductase gene and use thereof
; FILE REFERENCE: Levodione reductase
; CURRENT APPLICATION NUMBER: US/09/773,748
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: EP00101665.8
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Corynebacterium aquaticum
US-09-773-748-1

Query Match      22.4%; Score 293.5; DB 9; Length 267;
Best Local Similarity 31.8%; Pred. No. 6,9e-19;
Matches 84; Conservative 45; Mismatches 98; Indels 37; Gaps 9;

QY 12 VAVITGASGLGTAERLYVGGASAVLLDLPNSGGEQAKKIGNCFAP-----ADVT 66
DB 15 VVLTGGSGGLGRATRAVRLAEGAKLSLVDSSEGLESKAAVLETPADAEVLTIVADVS 74
QY 67 SEKDVOTATLALAKGFRGVDAVAVNCAIYASAKTYNLKQHTLEDFQRLVDVNLKGT 126
DB 75 DEAGVEAVYATTEFRGRIDGFENNAGIEGKQ-----NPTSEFTAAEDKIVYSINLRGVF 129
QY 127 ----NVITLVAGEMQNEPDGQGGVITINTASVAEFGVQGAAYSASKGIYGMTLPI 182
DB 130 LGLEKYLKIMR-----EAGS--GMVYNTASVGGIRGIGNSGYAAAKGAVGLRNS 179
QY 183 AADLAPIGIRVMTIAPGLFGLTSL-----PEKYC-NFLASQVFPFRLGDPAEY 233
DB 160 AVEYGRYGRIRMAIPGALIMPVNNSKKQDPEPRAAAEFFI--QVNPCKRYGEAPEI 237
QY 234 AHLVQAIEN--PFLNGEVRIDG 255
DB 238 AAVVAFLSDDASYVNAATVPIDG 261

; TYPE: PRT
; ORGANISM: Corynebacterium aquaticum
US-09-773-748-1
```

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RESULT 21
US-10-307-385-6
; Sequence 6, Application US/10307385
; Publication No. US2003007797A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZAKI, KENZO
; TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/10/307,385
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US/09/363,189
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Gluconobacter oxydans
US-10-307-385-6

Query Match      22.3%; Score 292.5; DB 9; Length 262;
Best Local Similarity 31.6%; Pred. No. 8,3e-19;
Matches 86; Conservative 41; Mismatches 110; Indels 35; Gaps 7;

QY 6 RSVKGLVAVITGASGLGTAERLYVGGASAVLLDLPNSG---GEQAKKIGNCFAP 62
DB 3 KRTNGKVCVLTGAGNGIATLRLAEBGTALALDMNNEALEKASVREKVEARSV 62
QY 63 ADVTSEKDVOTATLALAKGFRGVDAVAVNCAIYASAKTYNLKQHTLEDFQRLVDVL 122
DB 63 CDVTSEAVVIGTVDSVRDFGKIDLENNAGVGA-----FAPVDYPSDDFARVLTIV 117
QY 123 MGTENVIRLVAGEM-QONEPDGQGGVITINTASVAEFGVQGAAYSASKGIYGMTLP 181
DB 118 TGAFTVILKAASRQMTION-----YGRVTNTASVAGVGPMPMAAYGASKGAILIATBT 170
QY 182 IARDLAPIGIRVMTIAPGLF-----GTPILSLPEKYCNFLASQVFPFS 225
DB 171 AADLAPYINIRVAISPQVGPFWMERQVELOAKVGSQYFSDPRVVAQOMIGVPM-R 229
QY 226 RLGDPAEYAHVQAI--ENPFLNGEVRIDG 255
DB 230 RYGDINIRPGVAVAFILGDSDSFMVGNLPIAG 261

RESULT 22
US-09-802-853-6
; Sequence 6, Application US/09802853
; Patent No. US20010034049A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZAKI, KENZO
; TITLE OF INVENTION: XYLTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/09/802,853
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/363,189
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
```


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? PRIOR FILING DATE: 2000-11-27
? PRIOR APPLICATION NUMBER: 60/257,991
? PRIOR FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: 60/269,308
? PRIOR FILING DATE: 2001-02-16
? NUMBER OF SEQ ID NOS: 14110
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 13581
? LENGTH: 243
? TYPE: PR1
? ORGANISM: Streptococcus pneumoniae
? US-09-815-242-13581

```

[illegible]

```

RESULT 15
US-09-815-242-10921
; Sequence 10921, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Traxick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10921

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; LENGTH: 245
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10921

```

Query Match	24.3%;	Score	318.5;	DB	10;	Length	245;
Best Local Similarity	33.7%;	Pred. No.	3.3e-21;				
Matches	84;	Conservative	38;	Mismatches	108;	Indels	19;
						Gaps	5

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QY      15 ITGGASGLGATLERTLYVGGSAAVLLD-----LPSNGGEAOKKKJGNNCVAPADVSEKD  70
Db      10 ITSTRGIGAAVALAFAPAKAGATVINGNSEITPEORQETEA--FGVCIISLSDIEDPFA  67
QY      71 VGTALALAKKEFGRYDVAVNACAGIYASKTYNLKKQGTETLEDFQRYLVNLMGTENVIR  130
Db      68 AGEMIGATVDTLSIDILVNNAGIT-----NDKILLMTKEDEPNMACLDINTVGTENMQ  121
QY      131 LVAGEMQGNPNPDGGGGRGYIINTASAAPEGVGGGAASAKSGIYGMTPIARDLAPTIG  190
Db      122 QAAKRMKKQ-----BSGRITNMAASYGLMGVAGQANTAAKRAQVGFETTSVAREVAPRG  175
QY      191 IRVATITAGLEGTPLLTSLPERVCNFFLASQVPEFSRLCDPAEYVHLVQALITENPFLNGEY  250
Db      176 ITCAVIAAPGFIQEMTDIVLSEKVKQNMQNPLOT--FOVEDVAVATAIFLAKSPYITGOV  234
QY      251 IRLDGAIRM 259
Db      235 VAVDGGGLVM 243

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RESULT 16
US-10-175-696-14
; Sequence 14, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/662,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/505,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-696-14

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Query Match 24.08; Score 314; DB: 9; Length 237;

```
/ Patent No. US20020132319A1
/ GENERAL INFORMATION:
/ APPLICANT: ABREO, MELWYN A.
/ APPLICANT: AGREE, CHARLES S.
/ APPLICANT: AUGST, ROBERT
/ APPLICANT: KISSINGER, CHARLES R.
/ APPLICANT: MARGOSIAR, STEVE
/ APPLICANT: MENG, JERRY J.
/ APPLICANT: PELLETIER, LAURA A.
/ APPLICANT: REJTO, PAUL A.
/ APPLICANT: SHOWALTER, RICHARD E.
/ APPLICANT: TEMPCZYK-RUSSELL, ANNA
/ APPLICANT: THOMSON, JIM
/ APPLICANT: VANDERPOOL, DARIN
/ APPLICANT: VILIAFRANCA, J. ERNEST
/ TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
/ TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
/ TITLE OF INVENTION: OF INHIBITORS THEREOF
/ FILE REFERENCE: 0125-0049
/ CURRENT APPLICATION NUMBER: US/09/931,186
/ CURRENT FILING DATE: 2001-08-17
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 17
/ LENGTH: 259
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-931-186-17
```

```
Query Match 25.4%; Score 332.5; DB 10; Length 259;
Best Local Similarity 31.2%; Pred. No. 1.9e-22;
Matches 83; Conservative 51; Mismatches 105; Indels 27; Gaps 7;
```

```
QY 8 VNGVAVITGGASGLGATFAERLVQGSASAVLLDLPNSGGEAQAQKL-----GN 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 LRSALALVTGAGSGIGRAVSRLAGEATVAACDLDRAAAGETVRLGLGPPSKSGPPGN 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 57 NCFVAPADVTSEKDVOTALAKKFGGR-VDVAVNCAGIAVASKTYNKKQOTHTLEDFQ 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 HAAAF-QADVSEARARCLLEQVQACFSRPPSVVYSCAIGTIDEFLHMS-----DWD 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 RVLVDNLGTFENVILVAGENGQNEPDGQGVIIINTASVAAFEGOVQOAAVSASKGI 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 KYIAVNLGTFPLVYQAAAGALVSN-----GCRGSIINISSTVKGKGNVGNINYASKAGV 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 VGMPLPIARDLAPIGIRVMTIAPGLFGPPLTSLPEKVCNPLASQVPPPSRLGDAEYAH 235
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 IGLFTQTAARELGRHGRICNSVLPGRIPMTQKVQKVDKITEMIPM-GHLGDEEDVAD 233
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 236 LVQ--AIIEENPLNGEVRILQGAIRM 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 234 VVAFLASEDSGITGTSTVEVTGGLFM 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 13
US-09-815-242-13360
/ Sequence 13360, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
```

```
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13360
/ LENGTH: 243
/ TYPE: PRF
/ ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360
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Query Match 24.9%; Score 326.5; DB 10; Length 243;
Best Local Similarity 35.1%; Pred. No. 6.2e-22;
Matches 88; Conservative 36; Mismatches 104; Indels 23; Gaps 6;
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```
QY 15 ITGASGLGATFAERLVQGSASAVLLDLPNSGGE-----AQAKKLGNNCFVAPADVTSE 68
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 10 ITGSSRGIGLAIHAKFQAQANIVL-----NSRGAISEBLLAEFSNYGIRVPIISGVSDP 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 KDVOTALAKKFGGRVDVAVNCAGIAVASKTYNKKQOTHTLEDFQRLVDNLGTFENV 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 66 ADKARMIDQAIETELGASVDVAVNNAGI--TODTLMKN---TEADEKYLKVLVTGAFNM 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 129 IRLVAGMGNENPDGQGVIIINTASVAAFEGOVQOAAVSASKGIIVGWTLPRIARDLP 188
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 TOSVL-----KPMKMRREGAIIINMSVGLMKNIGANVAAKADLIGFTKVAAREVAS 173
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 189 IGIIVMTAPGLGTFPLTSLPEKVCNPLASQVPPPSRLGDAEYAHVQAIIEENPLNG 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 174 RNIVVNIYAPGMEISDMTALISDKIKETLAQIPM-KEFGAQVADLVTFVLAGQDYLTG 232
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 249 EVIRLDGAIRM 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 233 CVIAIDGGLSN 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 14
US-09-815-242-13581
/ Sequence 13581, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
```

PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentl Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-983-966-245

Query Match 87.5%; Score 1146; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.7e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGGAQAKKLGNNCFAPADVTSEKDVQTALALAKGFGRYDAVNCAGI 94
DB 1 ASAVLLDLPNSGGGAQAKKLGNNCFAPADVTSEKDVQTALALAKGFGRYDAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLEDFOQRLVDVNLMTGFNVIRLVAGEMGONEPDGQGRVYIINTA 154
DB 61 AVASKTYNLKKGQHTLEDFOQRLVDVNLMTGFNVIRLVAGEMGONEPDGQGRVYIINTA 120
QY 155 SVAAFEGVQGAAYASASKGIGVMTLPRIARDLAPIGIRVMTIAPGLGTPLTSLPEKVC 214
DB 121 SVAAFEGVQGAAYASASKGIGVMTLPRIARDLAPIGIRVMTIAPGLGTPLTSLPEKVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHVQAIENPFLNGEVIRLDGAIKMP 261
DB 181 NFLASQVPPPSRLGDPAEYAHVQAIENPFLNGEVIRLDGAIKMP 227

RESULT 10

US-10-143-090-245
Sequence 245, Application US/10143090
Publication No. US20030069406A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentl Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT

ORGANISM: Homo sapiens
US-10-143-090-245

Query Match 87.5%; Score 1146; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.7e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAVLLDLPNSGGGAQAKKLGNNCFAPADVTSEKDVQTALALAKGFGRYDAVNCAGI 94
DB 1 ASAVLLDLPNSGGGAQAKKLGNNCFAPADVTSEKDVQTALALAKGFGRYDAVNCAGI 60
QY 95 AVASKTYNLKKGQHTLEDFOQRLVDVNLMTGFNVIRLVAGEMGONEPDGQGRVYIINTA 154
DB 61 AVASKTYNLKKGQHTLEDFOQRLVDVNLMTGFNVIRLVAGEMGONEPDGQGRVYIINTA 120
QY 155 SVAAFEGVQGAAYASASKGIGVMTLPRIARDLAPIGIRVMTIAPGLGTPLTSLPEKVC 214
DB 121 SVAAFEGVQGAAYASASKGIGVMTLPRIARDLAPIGIRVMTIAPGLGTPLTSLPEKVC 180
QY 215 NFLASQVPPPSRLGDPAEYAHVQAIENPFLNGEVIRLDGAIKMP 261
DB 181 NFLASQVPPPSRLGDPAEYAHVQAIENPFLNGEVIRLDGAIKMP 227

RESULT 11

US-09-920-923-41
Sequence 41, Application US/09920923
Publication No. US20030022273A1
GENERAL INFORMATION:
APPLICANT: Tsyankev, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid
CURRENT APPLICATION NUMBER: US/09/920,923
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentl Ver. 2.1
SEQ ID NO 41
LENGTH: 388
TYPE: PRT
ORGANISM: Flavobacterium sp. R1534
US-09-920-923-41

Query Match 50.8%; Score 664.5; DB 9; Length 388;
Best Local Similarity 55.5%; Pred. No. 2.6e-52;
Matches 141; Conservative 35; Mismatches 69; Indels 9; Gaps 3;

QY 8 VKGLVAVITGGASGLGLATIERLVGGASAVLLDLPNSGGGAQAKKLGNNCFAPADVT 67
DB 143 IEGRVAVVTVGAASGLGASARMLAOGAKVYIADL-----AEPDAEGAVHAACVTD 196
QY 68 EKVQVRLALAKGKFGRYDAVNCAGIYASKTYNLKKGQHTLEDFOQRLVDVNLMTGFN 127
DB 197 ATAAQTALADNDRFERLDGLVNCAGIAPAEK--LGRDGPGLDSFARAAYTINLIGSN 254
QY 128 VIRLVAGEMGONEPDGQGRVYIINTASVAAREGVOGAAYASASKGIGVMTLPRIARDL 187
DB 255 MARLAAPARNPVR-GERGVYVNTASIAADQGLGQVAYASAGVAGMTLPARDA 313
QY 188 PIGIRVMTIAPGLGTPLTSLPEKVCNFLASQVPPPSRLGDPAEYAHVQAIENPFLN 247
DB 314 RHGIRVMTIAPGLGTPLTSLPEKVCNFLASQVPPPSRLGDPAEYAHVQAIENPFLN 373
QY 248 GEVIRLDGAIKMP 261
DB 374 GEVIRLDGAIKMP 387

RESULT 12

US-09-931-186-17
Sequence 17, Application US/09931186

Thu Jun 26 06:55:11 2003

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Page 5

Best Local Similarity 100.0%; Pred. No. 2.7e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAVILDLPSNGSGEAOAKKLGNNCVFAPADVTSEKDVQTLALAKGFGVAVVAVNCAGI 94
DB 1 ASAVILDLPSNGSGEAOAKKLGNNCVFAPADVTSEKDVQTLALAKGFGVAVVAVNCAGI 60
QY 95 AVASKTYNLKKGQTHLEDFORVLDVNLGTFENVIRLVAGENGQNEPDGQGRGVIIINTA 154
DB 61 AVASKTYNLKKGQTHLEDFORVLDVNLGTFENVIRLVAGENGQNEPDGQGRGVIIINTA 120
QY 155 SVAAFEGOVGOAAVSASKSGIVGMLPIARDLAPIGIRVWTIAPGLFTPLTSLPEKVC 214
DB 121 SVAAFEGOVGOAAVSASKSGIVGMLPIARDLAPIGIRVWTIAPGLFTPLTSLPEKVC 180
QY 215 NFLASQVPPPSRLGDPAEVAHLVQALIEENFLNGEVIIRLDGAIKMP 261
DB 181 NFLASQVPPPSRLGDPAEVAHLVQALIEENFLNGEVIIRLDGAIKMP 227

RESULT 8
US-09-966-262-245
Sequence 245, Application US/09966262
Publication No. US20030050461A1

GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 87 Human Secreted Proteins

FILE REFERENCE: P2004P1

CURRENT APPLICATION NUMBER: US/09/966, 262

PRIOR FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: US 09/154, 707

PRIOR FILING DATE: 1998-09-17

PRIOR APPLICATION NUMBER: PCT/US98/05311

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: US 60/041, 277

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/042, 344

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/041, 276

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/041, 281

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/048, 094

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 350

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 188

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 135

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/050, 937

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 187

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 099

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 352

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 186

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 069

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 095

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 131

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 096

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 355

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 160

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048, 154
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054, 804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056, 370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060, 862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 245
LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapiens
US-09-966-262-245
Query Match 87.5%; Score 1146; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.7e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 ASAVILDLPSNGSGEAOAKKLGNNCVFAPADVTSEKDVQTLALAKGFGVAVVAVNCAGI 94
DB 1 ASAVILDLPSNGSGEAOAKKLGNNCVFAPADVTSEKDVQTLALAKGFGVAVVAVNCAGI 60
QY 95 AVASKTYNLKKGQTHLEDFORVLDVNLGTFENVIRLVAGENGQNEPDGQGRGVIIINTA 154
DB 61 AVASKTYNLKKGQTHLEDFORVLDVNLGTFENVIRLVAGENGQNEPDGQGRGVIIINTA 120
QY 155 SVAAFEGOVGOAAVSASKSGIVGMLPIARDLAPIGIRVWTIAPGLFTPLTSLPEKVC 214
DB 121 SVAAFEGOVGOAAVSASKSGIVGMLPIARDLAPIGIRVWTIAPGLFTPLTSLPEKVC 180
QY 215 NFLASQVPPPSRLGDPAEVAHLVQALIEENFLNGEVIIRLDGAIKMP 261
DB 181 NFLASQVPPPSRLGDPAEVAHLVQALIEENFLNGEVIIRLDGAIKMP 227

RESULT 9
US-09-983-966-245

Sequence 245, Application US/09983966

Publication No. US20030060619A1

GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 87 Human Secreted Proteins

FILE REFERENCE: P2004P1

CURRENT APPLICATION NUMBER: US/09/983, 966

PRIOR FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 09/154, 707

PRIOR FILING DATE: 1998-09-17

PRIOR APPLICATION NUMBER: PCT/US98/05311

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: US 60/041, 277

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/042, 344

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/041, 276

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/041, 281

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/048, 094

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 350

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 188

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 135

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/050, 937

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048, 187

PRIOR FILING DATE: 1997-05-30

Db 61 APADVTSEKDVCTALALAKGKGRVAVANCAGINASTYMLKKQCTHTLDFQAVLDV 120
QY 121 NMGTENVIRLVAGGEGQNEPDGGGQGVYIINTASVAALFEGVGQAAYSASKGIYGMTL 180
Db 121 NMGTENVIRLVAGGEGQNEPDGGGQGVYIINTASVAALFEGVGQAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRMTTAPGFGFPLTSLPEKVCNPLASQVPPPSRLGDPAEYAHLYQAI 240
Db 181 PIARDLAPIGIRMTTAPGFGFPLTSLPEKVCNPLASQVPPPSRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMQP 261
Db 241 IENPFLNGEVIRLDGAIKMQP 261

RESULT 6

US-09-931-186-2
; Sequence 2, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABBRO, MELWYN A.
; APPLICANT: AGREE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENY, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARTIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931.186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: full length mutant ERAB C214R
US-09-931-186-2

Query Match 99.1%; Score 1297; DB 10; Length 261;

Best Local Similarity 99.6%; Pred. No. 6.7e-110;

Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVYTTGASGLGATPRLVGGASAVLDELPSGSGEAKKKGNNCVF 60
Db 1 MAACRSYKGLVAVYTTGASGLGATPRLVGGASAVLDELPSGSGEAKKKGNNCVF 60
QY 61 APADVTSEKDVCTALALAKGKGRVAVANCAGIYASKTYNLKKGTHTLDFQAVLDV 120
Db 61 APADVTSEKDVCTALALAKGKGRVAVANCAGIYASKTYNLKKGTHTLDFQAVLDV 120
QY 121 NMGTENVIRLVAGGEGQNEPDGGGQGVYIINTASVAALFEGVGQAAYSASKGIYGMTL 180
Db 121 NMGTENVIRLVAGGEGQNEPDGGGQGVYIINTASVAALFEGVGQAAYSASKGIYGMTL 180
QY 181 PIARDLAPIGIRMTTAPGFGFPLTSLPEKVCNPLASQVPPPSRLGDPAEYAHLYQAI 240
Db 181 PIARDLAPIGIRMTTAPGFGFPLTSLPEKVCNPLASQVPPPSRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMQP 261
Db 241 IENPFLNGEVIRLDGAIKMQP 261

RESULT 7

US-09-984-245-245
; Sequence 245, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984.245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/134,707
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-245

Query Match 87.5%; Score 1146; DB 9; Length 227;

APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C5V
US-09-931-186-4

Query Match 99.2%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.4e-110;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQAARKLGNNCYF 60
DB 1 MAAAVRSYKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQAARKLGNNCYF 60
QY 61 APADVTSEKDVOTATLAKKFGFRVDVAVNACGIAVASKTYNLKKGOTHTLEDFOYVLDV 120
DB 61 APADVTSEKDVOTATLAKKFGFRVDVAVNACGIAVASKTYNLKKGOTHTLEDFOYVLDV 120
QY 121 NLGTFENVIRLVAGEMQNEPDGQGRGVIINTASVAAEFGYQGAAYASAKSGIVGNTL 180
DB 121 NLGTFENVIRLVAGEMQNEPDGQGRGVIINTASVAAEFGYQGAAYASAKSGIVGNTL 180
QY 181 PIARDLAPIGIRVMTAPGLFTPLTSLPEKVCNFLASQVPPFSRLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTAPGLFTPLTSLPEKVCNFLASQVPPFSRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMQP 261
DB 241 IENPFLNGEVIRLDGAIKMQP 261

RESULT 4
US-09-931-186-6
Sequence 6, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 261
TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C58V
US-09-931-186-6

Query Match 99.2%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.4e-110;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQAARKLGNNCYF 60
DB 1 MAAACRSYKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQAARKLGNNCYF 60
QY 61 APADVTSEKDVOTATLAKKFGFRVDVAVNACGIAVASKTYNLKKGOTHTLEDFOYVLDV 120
DB 61 APADVTSEKDVOTATLAKKFGFRVDVAVNACGIAVASKTYNLKKGOTHTLEDFOYVLDV 120
QY 121 NLGTFENVIRLVAGEMQNEPDGQGRGVIINTASVAAEFGYQGAAYASAKSGIVGNTL 180
DB 121 NLGTFENVIRLVAGEMQNEPDGQGRGVIINTASVAAEFGYQGAAYASAKSGIVGNTL 180
QY 181 PIARDLAPIGIRVMTAPGLFTPLTSLPEKVCNFLASQVPPFSRLGDPAEYAHLYQAI 240
DB 181 PIARDLAPIGIRVMTAPGLFTPLTSLPEKVCNFLASQVPPFSRLGDPAEYAHLYQAI 240
QY 241 IENPFLNGEVIRLDGAIKMQP 261
DB 241 IENPFLNGEVIRLDGAIKMQP 261

RESULT 5
US-09-931-186-23
Sequence 23, Application US/09931186
Patent No. US20020132319A1
GENERAL INFORMATION:
APPLICANT: ABBRO, MELWYN A.
APPLICANT: AGREE, CHARLES S.
APPLICANT: AUST, ROBERT
APPLICANT: KISSINGER, CHARLES R.
APPLICANT: MARGOSIAK, STEVE
APPLICANT: MENG, JERRY J.
APPLICANT: PELLETIER, LAURA A.
APPLICANT: REJTO, PAUL A.
APPLICANT: SHOWALTER, RICHARD E.
APPLICANT: TEMPCZYK-RUSSELL, ANNA
APPLICANT: THOMSON, JIM
APPLICANT: VANDERPOOL, DARIN
APPLICANT: VILLAFRANCA, J. ERNEST
TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
TITLE OF INVENTION: OF INHIBITORS THEREOF
FILE REFERENCE: 0125-0049
CURRENT APPLICATION NUMBER: US/09/931,186
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 261
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: full length mutant ERAB C214S
US-09-931-186-23

Query Match 99.2%; Score 1299; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 4.4e-110;
Matches 260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAACRSYKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQAARKLGNNCYF 60
DB 1 MAAACRSYKGLVAVITGASGLGATAEERLVGGASAVLLDLPNSGGEAQAARKLGNNCYF 60
QY 61 APADVTSEKDVOTATLAKKFGFRVDVAVNACGIAVASKTYNLKKGOTHTLEDFOYVLDV 120

53 233 17.8 311 9 US-09-738-626-3819 Sequence 3819, Ap
94 231 17.6 261 10 US-09-815-242-5813 Sequence 5813, Ap
95 225.5 17.2 247 10 US-09-815-242-11342 Sequence 11342, A
96 224 17.1 254 10 US-09-741-669-411 Sequence 411, App
97 222.5 17.0 247 10 US-09-815-242-11514 Sequence 11514, A
98 223.5 17.0 900 9 US-10-060-230-15 Sequence 15, Appl
99 222.5 17.0 900 9 US-10-060-230-17 Sequence 17, Appl
100 216.5 16.3 253 10 US-09-815-242-10279 Sequence 10279, A

ALIGNMENTS

RESULT 1
US-09-931-186-8
; Sequence 8, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELWYN A.
; APPLICANT: AGREE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 261
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: wild type ERAB
US-09-931-186-8

Query Match 100.0%; Score 1309; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 5.4e-111;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACRSYKGLVAVITGASGLGATAEIRLVGGASAVLLDLPNSGGEQAOKKLGNCVF 60
DB 1 MAACRSYKGLVAVITGASGLGATAEIRLVGGASAVLLDLPNSGGEQAOKKLGNCVF 60
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RESULT 2

US-09-931-186-20
; Sequence 20, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELWYN A.
; APPLICANT: AGREE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCZYK-RUSSELL, ANNA
; APPLICANT: THOMSON, JIM
; APPLICANT: VANDERPOOL, DARIN
; APPLICANT: VILLAFRANCA, J. ERNEST
; TITLE OF INVENTION: PEPTIDE MUTANT OF HUMAN ERAB/HADH2, ITS X-RAY CRYSTAL
; TITLE OF INVENTION: STRUCTURE, AND MATERIALS AND METHOD FOR IDENTIFICATION
; FILE REFERENCE: 0125-0049
; CURRENT APPLICATION NUMBER: US/09/931,186
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 261
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length mutant ERAB C214A
US-09-931-186-20

Query Match 99.3%; Score 1300; DB 10; Length 261;
Best Local Similarity 99.6%; Pred. No. 3.6e-110;
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DB 181 PIARDLAPIGIRMTIAPGLFGFTPLTSLPEKVCNFIASQVPPSRLDPAEYAHLYOAI 240
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DB 241 IENPFLNGEVIIRLDGAIKMP 261

RESULT 3
US-09-931-186-4
; Sequence 4, Application US/09931186
; Patent No. US20020132319A1
; GENERAL INFORMATION:
; APPLICANT: ABREO, MELWYN A.
; APPLICANT: AGREE, CHARLES S.
; APPLICANT: AUST, ROBERT
; APPLICANT: KISSINGER, CHARLES R.
; APPLICANT: MARGOSIAK, STEVE
; APPLICANT: MENG, JERRY J.
; APPLICANT: PELLETIER, LAURA A.
; APPLICANT: REJTO, PAUL A.
; APPLICANT: SHOWALTER, RICHARD E.
; APPLICANT: TEMPCZYK-RUSSELL, ANNA

Thu Jun 26 06:55:11 2003

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OM protein - protein search, using sw model

Run on: June 23, 2003, 14:32:58 ; Search time 20.333 Seconds

(Without alignments)
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Title: US-09-931-186-8

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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